

1 ATGGCTGAGCTAGCGTGACCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC 60

Db 1 ATGAGCTGACGTAGCGTGAACCCCTGCTCCCTGAGTGTCTACAGCCCGGCTTCTCC 60
 QY 61 AAGACCTCTCTGGGAGCAAGCTGAAAGCCAGTACCTGTCTCCGCTGACAGAAACCTC 120
 Db 61 AAGACCTCTCTGGGAGCAAGCTGAAAGCCAGTACCTGTCTCCGCTGACAGAAACCTC 120
 QY 121 CTGCGACAGGCTTCCAGGCGCAGTGTGGCAACCGGTACTGTCTTCTGCTGCGCAC 180
 Db 121 CTGCGACAGGCTTCCAGGCGCAGTGTGGCAACCGGTACTGTCTTCTGCTGCGCAC 180
 QY 181 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGTCTGTCTTCAAGAGGGCATATATGAAGA 240
 Db 181 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGTCTGTCTTCAAGAGGGCATATATGAAGA 240
 QY 241 GGCATTCTTATTTTGAAGACGCTTGGCTTCCAGATATATGCTGCCGACAGGAGGTG 300
 Db 241 GGCATTCTTATTTTGAAGACGCTTGGCTTCCAGATATATGCTGCCGACAGGAGGTG 300
 QY 301 GAGAGCTGCGCGGCGCTGTCTCCAGATATGATGACCTGGAAGGAGGAGCCCTGAAGA 360
 Db 301 GAGAGCTGCGCGGCGCTGTCTCCAGATATGATGACCTGGAAGGAGGAGCCCTGAAGA 360
 QY 361 TACGAGTTTACGAGACCGTCAAGACTGTGGCAAGTGTGCAAGTCCCTTGCAGATTCCAC 420
 Db 361 TACGAGTTTACGAGACCGTCAAGACTGTGGCAAGTGTGCAAGTCCCTTGCAGATTCCAC 420
 QY 421 GCCATCGGCTGCTCCAGACGCTGAGAGGCTGAGAAACACGACAGAGACGAGGTGACGTG 480
 Db 421 GCCATCGGCTGCTCCAGACGCTGAGAGGCTGAGAAACACGACAGAGACGAGGTGACGTG 480
 QY 481 CTGCGGAGACGCTGCGCATGTACTGAGCTCGTCTGAGAGGCAAGCCCTCTTGGGA 540
 Db 481 CTGCGGAGACGCTGCGCATGTACTGAGCTCGTCTGAGAGGCAAGCCCTCTTGGGA 540
 QY 541 GACCAAGACCGCGGGGCTGAGCTCTCTGACAGAGTGTGAGAGCTTGGAGAAAGAGAG 600
 Db 541 GACCAAGACCGCGGGGCTGAGCTCTCTGACAGAGTGTGAGAGCTTGGAGAAAGAGAG 600
 QY 601 GCCACTTTTGAAGAACTTGTCTGCTCTGAGACCGGAGAGTGTGAGAGGCTGAGCA 660
 Db 601 GCCACTTTTGAAGAACTTGTCTGCTCTGAGACCGGAGAGTGTGAGAGGCTGAGCA 660
 QY 661 GCCGAGGCTGACCGCGGACGACCGCTGTGACCAAGACAAAGATTGAAGCCCTGAGTAC 720
 Db 661 GCCGAGGCTGACCGCGGACGACCGCTGTGACCAAGACAAAGATTGAAGCCCTGAGTAC 720
 QY 721 AAGGTGACAGAGCTGAGAGAGAGTGTGCTGACAGAGCTGCGAGTGTGAGTGTGAG 780
 Db 721 AAGGTGACAGAGCTGAGAGAGAGTGTGCTGACAGAGCTGCGAGTGTGAGTGTGAG 780
 QY 781 CAGAGAGTCTTGGAGATGAGAGGATCCACTACGATGAGGCTCTTCACTGGAAGATCTCA 840
 Db 781 CAGAGAGTCTTGGAGATGAGAGGATCCACTACGATGAGGCTCTTCACTGGAAGATCTCA 840
 QY 841 GACTTGGCGAGAAAGCTTCCAGAGAGTGTGCTGCGCGCATACCGGCTCTTCTCCCA 900
 Db 841 GACTTGGCGAGAAAGCTTCCAGAGAGTGTGCTGCGCGCATACCGGCTCTTCTCCCA 900
 QY 901 GACTTGGCGAGAAAGCTTCCAGAGAGTGTGCTGCGCGCATACCGGCTCTTCTCCCA 960
 Db 901 GACTTGGCGAGAAAGCTTCCAGAGAGTGTGCTGCGCGCATACCGGCTCTTCTCCCA 960
 QY 961 GGCACCGGCGGAGAAACACCTGTCTCTTCTTGTGTGATGAGAGGCGCGGATGAC 1020
 Db 961 GGCACCGGCGGAGAAACACCTGTCTCTTCTTGTGTGATGAGAGGCGCGGATGAC 1020
 QY 1021 GGCCTGTGCGGTGGGCTTCAACAGAGAGTGTATGCTGTGCTGACAGAGATAC 1080
 Db 1021 GGCCTGTGCGGTGGGCTTCAACAGAGAGTGTATGCTGTGCTGACAGAGATAC 1080
 QY 1081 CGGAGACGCTGATGACGCTTCAAGGCGCGAGTGAATCTCTCTTTTCAAGAGCCA 1140
 Db 1081 CGGAGACGCTGATGACGCTTCAAGGCGCGAGTGAATCTCTCTTTTCAAGAGCCA 1140

QY 1141 GTCAACGACATGAAATGCGAAGCGGCTGCCCTCTTCTGCCCCGCTCTCAAGATGAG 1200
 Db 1141 GTCAACGACATGAAATGCGAAGCGGCTGCCCTCTTCTGCCCCGCTCTCAAGATGAG 1200
 QY 1201 GCAAGAAATTCCTACGCGCGGAGAGATGATCTTCAATCAAGGCGATGAGACCTGACA 1260
 Db 1201 GCAAGAAATTCCTACGCGCGGAGAGATGATCTTCAATCAAGGCGATGAGACCTGACA 1260
 QY 1261 GGGCTCTTAA 1269
 Db 1261 GGGCTCTTAA 1269
 RESULT 2
 HSM806365
 LOCUS
 DEFINITION Homo sapiens mRNA; cDNA DKFP686H1465 (from clone DKFP686H1465); complete cds.
 ACCESSION BX538160
 VERSION BX538160.1 GI:31874595
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2244)
 AUTHORS Otenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W., Well, B., Amid, C., Oesinger, A., Fodor, G., Han, M., and Wiemann, S.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY
 COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; Sequenced by Medigenomix (Martinriedel/Germany) within the CDNA Sequencing Consortium of the German Genome Project. This clone (DKFP686H1465) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de. Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cdna/>.
 FEATURES
 source
 1..2244
 /organism="Homo sapiens"
 /mol_type="RNA"
 /db_xref="taxon:9606"
 /map="934.1"
 /clone="DKFP686H1465"
 /tissue_type="human endometrium"
 /clone_id="686 (synonym: hlc3). Vector pSport1_Sfi; host DH10B; sites SfiI + SfiIb
 /dev stage="adult"
 1..2244
 /gene="DKFP686H1465"
 <1..1505
 /gene="DKFP686H1465"
 /note="TNF receptor associated factor 2, differentially spliced"
 /product="hypothetical protein"
 /protein_id="CAD98040.1"
 /db_xref="GI:31874596"
 /translation="VAGRAISGRATVGNALPAGVTALMAAASVTPGSLBLIQPFS
 KTLGLYLENKYLCSACRNVLRRPFOAGGHRICSFCLASILSSGFQNCACVHBCIT
 EBOGILSSSSAPPDNNAREVBSLPAVCPDCTKGLKEYBSCHBGRCPMLTEC
 PCKGLVRLLEKEKRLHECEPERSLSRCRAPCCGADVFQDHFVTCCKRVPCEH
 AIGCLEFVEGKOEHEVQVREHMLMLSSVLEAKPLDGSQSHASLLQRESLEK
 KTAFTFNVCLNREVERVAMTAEASRQHRDQDKIELASSVQOOLERSIGKDLAM
 ADLEKYLEWBSASTYGVFTWKISDPSARQEPVARIPIAPSPARVTSRYKMDLR
 IYLANGDTGKTHLSLPFVYMKSPDNLIRMPNQVYITMLDQNNREHYIDAFRDV
 TSSSFQRPVNDNMVIAAGCPICPVSTKELRNKSNVRRDPAIFKATVLTGL"
 2193..2198
 /gene="DKFP686H1465"
 poly_a_signal

REMARK
COMMENT

USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@gscc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan North,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabhu,
Parvaneh Saeedi, Jr Santos, Angeliq Schermer, Ursula Skalska,
Diane Smalls, Jeff Stott, Miranda Teal, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
Series: IRAC Plate: 89 Row: 3 Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 22027611.
location/Qualifiers

FEATURES

source

1..2298
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:49872 IMAGE:5767794"
/tissue_type="Brain, fetal, whole pooled"
/clone_lib="NIH MGC_121"
/lab_host="DH10B"
/note="Vector: PCMV-SPORE"
1..2298
/gene="TRAF2"
/note="synonyms: TRAF3, TRAF, MGC:45012"
/db_xref="LocusID:7186"
/db_xref="MIM:601895"
58..1563
/gene="TRAF2"
/codon_start=1
/product="TNF receptor-associated factor 2"
/protein_id="AAH43492.1"
/db_xref="GI:28175372"
/db_xref="LocusID:7186"
/db_xref="MIM:601895"
/translation="MAAASVTTPGSLIELDPGFSKTLTGLKLEAKYLSACANVLRP
FOQCHRYCSFLIASILSSGPONCAVHEGIYEGLSILSSSAFDPNARREVES
LPAVPSDGTWKGTLKEYESCHERCPMLTEPCXKLVRLEKHEKLEHECPERS
LSCRHRAPCCGADVAHNEVCPKPLTCDGCKKKIPEKFDQHVKTCGKORVCFE
HAIGLETVEGKOEHEVOMLEHMLSSVLEAKPLIGDSHAGSELJORCSLE
KKATPENIVCVINREVERVAMTAECQHRLLDODKIEALSSKYOOLERSIGKDLA
MDIPEKULMEASTYDGVETIKISDPARKROEAVAGTAPAIASFATSPRGYKML
RIYKNGDTGRTGTHLSLFVWVKGPRDALIRMPFNOKTITMLLDNNRBYVDARPD
VTSSTFRPVDNNTIASGCLPCPVSKMEAKNSYVRDNIIFKALVDLTGL"

CDS

gene

ORIGIN

Query Match 80.4%; Score 1020.4; DB 9; Length 2298;
Best Local Similarity 84.2%; Pred. No. 4e-202;
Matches 1268; Conservative 0; Mismatches 1; Indels 237; Gaps 1;

DB 1 ATGGCTGCAAGTACGCTGACCCCTGGCTCCCTGAGTTGCTACAGCCGGCTTTCTCC 60
DB 58 ATGGCTGCAAGTACGCTGACCCCTGGCTCCCTGAGTTGCTACAGCCGGCTTTCTCC 117
DB 61 AAGACCTCTGCGGGAACAAGCTGGAAGCAAGTACCTGTGCTCGGCGCGGAGAAAGC 120
DB 118 AAGACCTCTGCGGGAACAAGCTGGAAGCAAGTACCTGTGCTCGGCGCGGAGAAAGC 177
DB 121 CTCGAGAGCCCTTCCAGGCGCAAGTGTGCGCAACCGGTACTGCTCTTGTGCTGCGCAGC 180
DB 178 CTCGAGAGCCCTTCCAGGCGCAAGTGTGCGCAACCGGTACTGCTCTTGTGCTGCGCAGC 237

DB 181 ATCTCAAGCTCTGGAGCCTCAGAACTGTGCTGCTGTGTGTCACGAGGCAATATGAGAA 240
DB 228 ATCTCAAGCTCTGGAGCCTCAGAACTGTGCTGCTGTGTGTCACGAGGCAATATGAGAA 297
DB 241 GGCATTTCTATTTTGAAGAGAGTTCGGCTTCCCAATATATGTGTCGGCAGGAGAGTG 300
DB 298 GGCATTTCTATTTTGAAGAGAGTTCGGCTTCCCAATATATGTGTCGGCAGGAGAGTG 357
DB 301 GAGAGCTCGCGCCGCTGTGCTCCAGTATGATGATGACCTGGAAGGAGCACTTGAAGAA 360
DB 358 GAGAGCTCGCGCCGCTGTGCTCCAGTATGATGATGACCTGGAAGGAGCACTTGAAGAA 417
DB 361 TACG----- 364
DB 418 TACGAGAGCTTCACGAGAGCGCTGCCCTCATGCTGACCCGATGTCGGCGTGCAAA 477
DB 365 ----- 364
DB 478 GCGCTGCTCGCCTTGTGTGAAGAGAGCGCACCTGAGACAGAGTCCCGAGAGAGC 537
DB 365 ----- 364
DB 538 CTGAGCTGCGGCAATGTCGGGCACTCTGCTGCGGAGACAGAGTGAAGCGCACAGAG 597
DB 365 ----- 364
DB 598 GTCTGCCCCAAGTTCCTCCCTTAACCTTGTGACGCTGCGGCAAGAAAGATCCCGGAG 657
DB 365 -AGTTTGAAGACCAAGTCAAGACTTGTGCAAGTGTGAGTCCCTTGCAGATTCAAGCC 423
DB 658 AAGTTTGAAGACCAAGTCAAGACTTGTGCAAGTGTGAGTCCCTTGCAGATTCAAGCC 717
DB 424 ATCGCTGCTCTCGAGAGCTGTGAGAGGTGTGAGAAACAGAGAGACCAAGTGTGCTG 483
DB 718 ATCGCTGCTCTCGAGAGCTGTGAGAGGTGTGAGAAACAGAGAGACCAAGTGTGCTG 777
DB 484 CGGAGACCTGCGCATGCTACTGAGCTCGGTGTGAGAGCAAGCCCTTGTGAGAGAG 543
DB 778 CGGAGACCTGCGCATGCTACTGAGCTCGGTGTGAGAGCAAGCCCTTGTGAGAGAG 837
DB 544 CAGAGCAACGCGGCTGAGAGCTTCTGACAGAGTGTGAGAGCTTGTGAGAGAGAGCGCC 603
DB 838 CAGAGCAACGCGGCTGAGAGCTTCTGACAGAGTGTGAGAGCTTGTGAGAGAGAGCGCC 897
DB 604 ACTTTGAGAACTTGTCTGCTGCTGAGAACCGGGAAGTGTGAGAGAGGCTGAGCTGCC 663
DB 898 ACTTTGAGAACTTGTCTGCTGCTGAGAACCGGGAAGTGTGAGAGAGGCTGAGCTGCC 957
DB 664 GAGGCTGCAAGCCCGGCAAGCAACGCTGTGACCAAGCAAGATTGAAGCCCTGAGTACAG 723
DB 958 GAGGCTGCAAGCCCGGCAAGCAACGCTGTGACCAAGCAAGATTGAAGCCCTGAGTACAG 1017
DB 724 GTGAGAGCTGTGAGAGAGCACTTGGCTCAAGAGCTGTGCTGAGCTTGTGAGAGAG 783
DB 1018 GTGAGAGCTGTGAGAGAGCACTTGGCTCAAGAGCTGTGCTGAGCTTGTGAGAGAG 1077
DB 784 AAGTCTTGAAGATGAGAGGATCCACCTAGATGAGGCTTTCATCTGGAAGATCTCAGAG 843
DB 1078 AAGTCTTGAAGATGAGAGGATCCACCTAGATGAGGCTTTCATCTGGAAGATCTCAGAG 1137
DB 844 TTGCGCAGAAAGCTCCAGAAAGCTGTGAGCTGTGCGGCAATACCGGCACTTTCTCCAGAG 903
DB 1138 TTGCGCAGAAAGCTCCAGAAAGCTGTGAGCTGTGCGGCAATACCGGCACTTTCTCCAGAG 1197
DB 904 TTCTACACCAAGAGTACGCTCAAGATGTGTCTGATCTGATCTGAAACGCGAGAGCG 963
DB 1198 TTCTACACCAAGAGTACGCTCAAGATGTGTCTGATCTGATCTGAAACGCGAGAGCG 1257
DB 964 ACCGCGAGAGAAACAACCTGTCTCTTCTTTGTGTGTGATGAGAGGCGCGAATGACGCC 1023
DB 1258 ACCGCGAGAGAAACAACCTGTCTCTTCTTTGTGTGTGATGAGAGGCGCGAATGACGCC 1317

QY 1024 CTGCTGGGTGGCCCTTACACAGAGGTGACCTTAATGCTGCTGACACAGATAACCGG 1083
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1318 CTGCTGGGTGGCCCTTACACAGAGGTGACCTTAATGCTGCTGACACAGATAACCGG 1377
 QY 1084 GAGCAGCTGATTGACGCTTTACGCGCCGACGCTGACTTCATCTCTTTTCAGAGGCCAGTC 1143
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1378 GAGCAGCTGATTGACGCTTTACGCGCCGACGCTGACTTCATCTCTTTTCAGAGGCCAGTC 1437
 QY 1144 AAGCAGATGACATCGACGAGCGCTGCCCTCTTCTGCCCCGTCTCCCAAGATGAGAGCA 1203
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1438 AAGCAGATGACATCGACGAGCGCTGCCCTCTTCTGCCCCGTCTCCCAAGATGAGAGCA 1497
 QY 1204 AAGAAATCTTACCTGCGGGACGATGCATCTTCATCAAGGCCATTGTGACCTGACAGG 1263
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1498 AAGAAATCTTACCTGCGGGACGATGCATCTTCATCAAGGCCATTGTGACCTGACAGG 1557
 QY 1264 CTCTAA 1269
 Db |||||||
 1558 CTCTAA 1563
 RESULT 4
 BC032410
 LOCUS
 DEFINITION Homo sapiens TNF receptor-associated factor 2, mRNA (cDNA clone
 MGC:40274 IMAGE:5216790), complete cds.
 ACCESSION BC032410
 VERSION BC032410.1 GI:21619569
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE
 AUTHORS
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.C., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477922
 2 (bases 1 to 2307)
 Strausberg, R.
 Direct Submission
 Submitted (06-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgi.nih.gov>
 Contact: MGC help desk
 Email: cgabs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@hri.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lari, P., Legaspi, R.,
 Maduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 64 Row: 1 Column: 7
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 22027613.
 Location/Qualifiers

FEATURES

source

1..2307
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:40274 IMAGE:5216790"
 /tissue_type="Blood, adult leukocytes"
 /clone_lib="NIH MGC_118"
 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"
 1..2307
 /gene="TRAF2"
 /note="synonyms: TRAF3, TRAP, MGC:45012"
 /db_xref="LocusID:7186"
 /db_xref="MIM:601895"
 44..1549
 /gene="TRAF2"
 /codon_start=1
 /product="TNF receptor-associated factor 2"
 /protein_id="AAH32410.1"
 /db_xref="GI:21619570"
 /db_xref="LocusID:7186"
 /db_xref="MIM:601895"
 /translation="MAAASVTPPGSLLELPQPSKTLTGKLEAKVLCSCNRVLRPP
 FQAQCHRYGSPCLASILSGPONCAACVHEGIEGSILESSAPFONAAARREV
 LPVCSDDGTWGLKEVSECHGRCPLMLTECPACKGLRGLRKEHLEKCPERS
 LSRCHRAPCCGADVKAHEVCPFLPTCDGCKKIPREKFDQHVTKGCKRCPFR
 HAIGCLETVEGQKQHEVQWMLREHMLLSVLEAKPLIGDOSHAGLLQRCSELE
 KKTATFENIVCLNREVRVAMTAECASQRLDDOKIEALSSKVOQLERSIGLKDLA
 MADLEQKVMLEASTVDGFIWKISDFARKQEAAGRIPIAFSPAFYTSRYGKML
 RYLNGDGTGRGTHLSLFFVVMKGNPDALLRPPFNQKVTMLLDNNRHRVIDAFRPP
 VTSSSRQRPVNDNINIASGCLPFCFVSMKANSYVRDDAIFIKAVLDLTGL"

ORIGIN

Query Match 80.4%; Score 1020.4; DB 9; Length 2307;
 Best Local Similarity 84.3%; Pred. No. 4e-202;
 Matches 1268; Conservative 0; Mismatches 1; Indels 237; Gaps 1;
 QY 1 ATGGCTGCAGCTAGCGTACCCCTCCCTGGCTGCTGAGTTGTACAGCCGCGCTTCTCC 60
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 44 ATGGCTGCAGCTAGCGTACCCCTCCCTGGCTGCTGAGTTGTACAGCCGCGCTTCTCC 103
 QY 61 AAGACCCCTCTCTGGGGACCAAGCTGGAAGCAAGTACTGTGCTCCGCTGCAGAAACGTC 120
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 104 AAGACCCCTCTCTGGGGACCAAGCTGGAAGCAAGTACTGTGCTCCGCTGCAGAAACGTC 163
 QY 121 CTCGCGAGGCCCTTCCAGGCGAGTGTGGCCACCGGTACTGTCTCTCTGCTGGCCAGC 180
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 164 CTCGCGAGGCCCTTCCAGGCGAGTGTGGCCACCGGTACTGTCTCTCTGCTGGCCAGC 223
 QY 181 ATCTCTGAGCTCTGGGCTCTAGAACTGCTGCTGCTGCTTACAGAGGCATATATGAAGA 240
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 224 ATCTCTGAGCTCTGGGCTCTAGAACTGCTGCTGCTTACAGAGGCATATATGAAGA 283
 QY 241 GGCATTCTATTTTATAGAAAGCAGTTTCGGCTTCCACAGATAATGCTCCCGCGAGGGAGTG 300
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 284 GGCATTCTATTTTATAGAAAGCAGTTTCGGCTTCCACAGATAATGCTCCCGCGAGGGAGTG 343

QY 301 GAGAGCCTGCGGCGCTCTGTCCAGTGTGATGACCTGGAAGGGGACCCCTGAAGAA 360
 Db 344 GAGAGCCTGCGGCGCTCTGTCCAGTGTGATGACCTGGAAGGGGACCCCTGAAGAA 403
 QY 361 TAAG----- 364
 Db 404 TACGAGAGCTGCCACGAAGCGCTGCGCGCTCATGCTGACGAATGTCCCGGCTCAAA 463
 QY 365 ----- 364
 Db 464 GGCCTGTGCGCTTGTGTAAGAGAGCGCCACCTGGAGCACAGTGCCTGGAGAGAGC 523
 QY 365 ----- 364
 Db 524 CTGAGCTGCGGCGATTCGCGGCGACCTGCTGCGGAGACAGCTGAAGCGGACCAAGAG 593
 QY 365 ----- 364
 Db 584 GTCTGCCCAAGTTCCTCCCTAACTTTGTGACGGTGTGCGGCAAGAAAGATCCCCCGGAG 643
 QY 365 -AGTTTCAGGACCAAGTCAAGACTTTGTGCAAGTGTGAGTCCCTTTCAGATTCACGCG 423
 Db 644 AAGTTTCAGGACCAAGTCAAGACTTTGTGCAAGTGTGAGTCCCTTTCAGATTCACGCG 703
 QY 424 ATCGGCTGCTGAGAGCGGTAGAGGTGAGAAACAGAGAGCACGAGTGTGAGTGGCTG 483
 Db 704 ATCGGCTGCTGAGAGCGGTAGAGGTGAGAAACAGAGAGCACGAGTGTGAGTGGCTG 763
 QY 484 CGGAGAGCACTGGCCATCTACTAGTCTGCTGAGGCAAGCCCTTTCAGATTCACGCG 543
 Db 764 CGGAGAGCACTGGCCATCTACTAGTCTGCTGAGGCAAGCCCTTTCAGATTCACGCG 823
 QY 544 CAGAGCCACGCGGCTCAGAGCTCCTGACAGGTGTCGAGAGCTGAGAGAGAGAGAGCGCC 603
 Db 824 CAGAGCCACGCGGCTCAGAGCTCCTGACAGGTGTCGAGAGCTGAGAGAGAGAGAGCGCC 883
 QY 604 ACTTTGAGACATCTGCTGCTGCTGAGCGGAGTGTGAGAGGTGAGAGGTGAGAGTGGC 663
 Db 884 ACTTTGAGACATCTGCTGCTGCTGAGCGGAGTGTGAGAGGTGAGAGGTGAGAGTGGC 943
 QY 664 GAGGCTGACGCGGAGCAGCGCTGAGCAAGATTTGAAGCTTGAAGCTTGAAGCTTGAAG 723
 Db 944 GAGGCTGACGCGGAGCAGCGCTGAGCAAGATTTGAAGCTTGAAGCTTGAAGCTTGAAG 1003
 QY 724 GTGAGAGCTGAGAGAGAGATTTGGCTCAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 783
 Db 1004 GTGAGAGCTGAGAGAGAGATTTGGCTCAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1063
 QY 784 AAGGTCTTGGAGATGGAGGATCCACCTACGATGGGCTTTCATCTGGAAGATCTCAGAC 843
 Db 1064 AAGGTCTTGGAGATGGAGGATCCACCTACGATGGGCTTTCATCTGGAAGATCTCAGAC 1123
 QY 844 TTCGCCAGAGAGCTCCAGAGAGTGTGCTGCGCGCATACCGGCTTTCCTCCAGCC 903
 Db 1124 TTCGCCAGAGAGCTCCAGAGAGTGTGCTGCGCGCATACCGGCTTTCCTCCAGCC 1183
 QY 904 TTCTACACAGAGTACGCTTACAGAGTGTCTGCTGATCTACCTGGAAGAGAGAGCGG 963
 Db 1184 TTCTACACAGAGTACGCTTACAGAGTGTCTGCTGATCTACCTGGAAGAGAGAGCGG 1243
 QY 964 ACCGGGAGAGAAACACCTCTTCCTTGTGATGATGAGAGGCGCGAGATGAGCC 1023
 Db 1244 ACCGGGAGAGAAACACCTCTTCCTTGTGATGATGAGAGGCGCGAGATGAGCC 1303
 QY 1024 CTGCTGCGGCTGAGAGAGTGTGCTGCTGATGATGATGATGATGATGATGATGATGATG 1083
 Db 1304 CTGCTGCGGCTGAGAGAGTGTGCTGCTGATGATGATGATGATGATGATGATGATGATG 1363
 QY 1084 GAGCAGCTGATGAGCGCTTCAGGCGCGAGCTGATCTTCTCTCTCTCTCTCTCTCTCTCT 1143
 Db 1364 GAGCAGCTGATGAGCGCTTCAGGCGCGAGCTGATCTTCTCTCTCTCTCTCTCTCTCTCT 1423
 QY 1444 AACGACATGAATCGGAGCGGCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1203

Db 1424 AACGACATGAATCGGAGCGGCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1483
 QY 1204 AAGATTCTCAGTGTGCGGAGCGATGCGCATCTTCAAGGCGCATTTGGACCTGACAGGG 1263
 Db 1484 AAGATTCTCAGTGTGCGGAGCGATGCGCATCTTCAAGGCGCATTTGGACCTGACAGGG 1543
 QY 1264 CTCTAA 1269
 Db 1544 CTCTAA 1549

RESULT 5
 BC033810 2320 bp mRNA linear PRI 30-JUN-2004
 LOCUS Homo sapiens TNF receptor-associated factor 2, mRNA (cDNA clone
 DEFINITION MGC:45012 IMAGE:5182942); complete cds.
 ACCESSION BC033810
 VERSION BC033810.1 GI:21708063
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2320)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Shat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Dietzenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, D.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzyzanski, M.I., Skalska, J., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 2320)
 Strausberg, R.
 Direct Submission
 Submitted (02-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgpbbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nih.gov
 Akher, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Grant, S., Guan, X., Gupta, J., Hachiguchi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantrisp, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAK Plate: 68 Row: 1 Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22027611.

FEATURES

Location/Qualifiers
1..2320
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:45012 IMAGE:5182942"
/issue_type="Colon, Kidney, Stomach, adult, whole pooled"
/clone_lib="NIH MGC_116"
/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6"
1..2320
/gene="TRAF2"
/note="synonyms: TRAF3, TRAF, MGC:45012"
/db_xref="LocusID:7186"
/db_xref="MIM:601895"
46..1551
/gene="TRAF2"
/codon_start=1
/product="TNF receptor-associated factor 2"
/protein_id="AAH33810.1"
/db_xref="GI:21708064"
/db_xref="LocusID:7186"
/db_xref="MIM:601895"
/translation="MAAASVTPPGSLLELPQFSLTLLGKLEAKYLCASACNVLRRP
FOAQCHRYCSFLASIISSGPNCAACVHEGIEGSIILESSAPFNHAECPERS
LPAVCPDQCTWKTGLKEVSECHGRCPLMLTECPACKGLVRLGKRLHECPERS
LSRCRAPCCGADVAHVEVCPFLPCDGGKKIIPREKFOHVTKCGKRVCPFR
HAIGLETVGKQEHVEVRLHMLLSVLEAKPLDGGSHAGSELQRCESLE
KTAFTENIVCLNREVERNTAACSRRQRLDQKIEALSSKVQQLSRLSGLKDLA
MADLQKVLMEASTYDGVFIWIKISDFARKQEA VAGRI PAI FSPAFYTSRYGMCL
RYLNGDGTGHTLSLFLFVVMKGNDFALLRPFNQKVTLMLLDQNRHRYDAFRPD
VTSSFRQPVNDMNIASGCLFPCVPKMEAKNSVYRDDAIFIKAIVDLTGL"

ORIGIN

Query Match 80.4%; Score 1020.4; DB 9; Length 2320;
Best Local Similarity 84.2%; Pred. No. 4e-202;
Matches 1268; Conservative 0; Mismatches 1; Indels 237; Gaps 1;
1 ATGGCTGACGTAGCGTGACCCCGCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC 60
46 ATGGCTGACGTAGCGTGACCCCGCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC 105
61 AAGACCTCTCTGGGACCAAGTGAAGCAAGTACCTGTGCTCCGCTGAGAAACGTC 120
106 AAGACCTCTCTGGGACCAAGTGAAGCAAGTACCTGTGCTCCGCTGAGAAACGTC 165
121 CTCGCGAGCCCTCCAGCGCAGTGTGGCCACCGTACTGCTCTTCTGCTGGCCAGC 180
166 CTCGCGAGCCCTCTCAGCGCAGTGTGGCCACCGTACTGCTCTTCTGCTGGCCAGC 225
181 ATCTCAGCTCTGGGCTCAGAACCTGTGCTGCTGTGCTACGAGGCGATATATGAAGAA 240
226 ATCTCAGCTCTGGGCTCAGAACCTGTGCTGCTGTGCTACGAGGCGATATATGAAGAA 285
241 GCAATTTCTATTAGAAAGAGTGTGGCTTCCAGATATGCTGCCCGGAGGAGGTG 300
286 GCAATTTCTATTATAGAAAGAGTGTGGCTTCCAGATATGCTGCCCGGAGGAGGTG 345
301 GAGAGCTGCGGCGCTGTGCTCCAGTGTGATGATGATGATGATGATGATGATGATGATG 360
346 GAGAGCTGCGGCGCTGTGCTCCAGTGTGATGATGATGATGATGATGATGATGATGATG 405
361 TAGC-----
406 TACGAGAGTGCCAGAGGCGGTGCCCGCTCATGTGCTGACCGAATGTCCCGCGTCAAA 465
365 -----

Db 466 GGCCTGGTTCGGCTTGGTGAAGAGGAGCGCCACCTGAGCAGCAGTGCCTCGGAGAGAAGC 525
Qy 365 ----- 364
Db 526 CTGAGTGCCTGGCATTGTCGGGACACCTCTGTCGGGAGCAGACGTGAAGGCGCACACGAG 585
Qy 365 ----- 364
Db 586 GTCTGCCCCAAGTTCCTTTAACTTGTGCGGCTGCGGCAAGAAAGATCCCCCGGGAG 645
Qy 365 -AGTTTCAGGACACAGTCAAGACTTGTGGCAAGTGTGAGTCCCTTTCAGATTCACGCG 423
Db 646 AAGTTTCAGGACACAGTCAAGACTTGTGGCAAGTGTGAGTCCCTTTCAGATTCACGCG 705
Qy 424 ATCGCTGCTTCGAGACGCTAGAGGTGAGAAACAGCAGGAGCAGCAGGTGTCAGTGGCTG 483
Db 706 ATCGCTGCTTCGAGACGCTAGAGGTGAGAAACAGCAGGAGCAGCAGGTGTCAGTGGCTG 765
Qy 484 CGGAGCACCTGGCCATGCTACTGAGCTCGGTGCTGGAGCAAGCCCTCTTTGGGAGAC 543
Db 766 CGGAGCACCTGGCCATGCTACTGAGCTCGGTGCTGGAGCAAGCCCTCTTTGGGAGAC 825
Qy 544 CAGAGCCACCGGGGTGAGAGCTCTGAGCTCGGTGCTGGAGCAAGCCCTCTTTGGGAGAC 603
Db 826 CAGAGCCACCGGGGTGAGAGCTCTGAGCTCGGTGCTGGAGCAAGCCCTCTTTGGGAGAC 885
Qy 604 ACTTTTGAGAACATTGTCTGCTGCTGCTGACCCGGAGGTGAGAGGCTGGCCATGACTGCC 663
Db 886 ACTTTTGAGAACATTGTCTGCTGCTGCTGACCCGGAGGTGAGAGGCTGGCCATGACTGCC 945
Qy 664 GAGCCTGACCGGGAGACCCGCTGGACCAAGACCAAGATTGAGCCCTGAGTAGCAAG 723
Db 946 GAGCCTGACCGGGAGACCCGCTGGACCAAGACCAAGATTGAGCCCTGAGTAGCAAG 1005
Qy 724 GTGAGCAGCTGGAGAGGAGCATTGGCTCAAGAGACCTGGCGATGGCTGACTTGGAGCAG 783
Db 1006 GTGAGCAGCTGGAGAGGAGCATTGGCTCAAGAGACCTGGCGATGGCTGACTTGGAGCAG 1065
Qy 784 AAGTCTTGAGATGAGAGGATCCACTAGATGGGTCTTCACTGGAAGATCTCAGAC 843
Db 1066 AAGTCTTGAGATGAGAGGATCCACTAGATGGGTCTTCACTGGAAGATCTCAGAC 1125
Qy 844 TTGCCAGGAGGCTCCAGGAGGCTGTGGCTGGCGGATACCCGCCATCTTCTCCCGAGCC 903
Db 1126 TTGCCAGGAGGCTCCAGGAGGCTGTGGCTGGCGGATACCCGCCATCTTCTCCCGAGCC 1185
Qy 904 TTCTACACAGCAGGTACCGCTACAGATGTGTCTGCTATCTACCTGAACGCGCAGCGC 963
Db 1186 TTCTACACAGCAGGTACCGCTACAGATGTGTCTGCTATCTACCTGAACGCGCAGCGC 1245
Qy 964 ACCGGGCGAGAACACACCTGTCCCTCTTTTGTGGTATGAAGGCCCGAATGAGCC 1023
Db 1246 ACCGGGCGAGAACACACCTGTCCCTCTTTTGTGGTATGAAGGCCCGAATGAGCC 1305
Qy 1024 CTGCTGGGTGGCCCTTTCAACACAGAGGTGACCTTAATGTCTCGACAGATAACCGG 1083
Db 1306 CTGCTGGGTGGCCCTTTCAACACAGAGGTGACCTTAATGTCTCGACAGATAACCGG 1365
Qy 1084 GAGCAGTGTATTGAGCGCTTCAGGCCCGAGCTGACTTCCTCTTTTTCAGAGCCAGTC 1143
Db 1366 GAGCAGTGTATTGAGCGCTTCAGGCCCGAGCTGACTTCCTCTTTTTCAGAGCCAGTC 1425
Qy 1144 AAGCAGATGAACATCGAAGCGGCTGCCCTCTTCTGCGCCCGTCTCCAAAGATGAGGCA 1203
Db 1426 AAGCAGATGAACATCGAAGCGGCTGCCCTCTTCTGCGCCCGTCTCCAAAGATGAGGCA 1485
Qy 1204 AAGAAATCTTACCTGGGAGCAGATGCTATCTTCAAGAGCCATTTGTGACCTGACAGG 1263
Db 1486 AAGAAATCTTACCTGGGAGCAGATGCTATCTTCAAGAGCCATTTGTGACCTGACAGG 1545
Qy 1264 CTCTAA 1269
|||||


```
Db 713 ATCGGTGCTCGAGACGGTAGAGGGTGAGAAACAGCAGGACGACGAGGTGAGTGGTGT 772
QY 484 CGGGACACCTGGCCCTGCTACTAGACTCGGTGCTGGAGGCAAGCCCTCTTTGGAGAC 543
Db 773 CGGGACACCTGGCCCTGCTACTAGACTCGGTGCTGGAGGCAAGCCCTCTTTGGAGAC 832
QY 544 CAGAGCCACGCGGGTCAAGAGTCTCTGAGAGGTGCGAGAGCTCGAGAGCAAGCGCC 603
Db 833 CAGAGCCACGCGGGTCAAGAGTCTCTGAGAGGTGCGAGAGCTCGAGAGCAAGCGCC 892
QY 604 ACTTTTGAGAACATTTCTGCGTCTCTGACCGGAGGTGAGAGGTGCGCATGACTGCC 663
Db 893 ACTTTTGAGAACATTTCTGCGTCTCTGACCGGAGGTGAGAGGTGCGCATGACTGCC 952
QY 664 GAGGCTGACGCGGCGAGCACCGGTGGACCAAGCAAGATTGAAGCCCTGAGTAGCAAG 723
Db 953 GAGGCTGACGCGGCGAGCACCGGTGGACCAAGCAAGATTGAAGCCCTGAGTAGCAAG 1012
QY 724 GTGCACAGCTGGAGAGGACATGGCCCTCAGGACCTGGCGATGGCTGACTTGGAGAG 783
Db 1013 GTGCACAGCTGGAGAGGACATGGCCCTCAGGACCTGGCGATGGCTGACTTGGAGAG 1072
QY 784 AAGGTCTTGGAGATGAGAGCATCCACCTACGATGGGTCTTCTATCTGGAAGATCTCAGAC 843
Db 1073 AAGGTCTTGGAGATGAGAGCATCCACCTACGATGGGTCTTCTATCTGGAAGATCTCAGAC 1132
QY 844 TTGCGCAGGAAGTCCAGGAAGTGTGGCTGGCGGACATACCGCATCTTCTCCCGAGCC 903
Db 1133 TTGCGCAGGAAGTCCAGGAAGTGTGGCTGGCGGACATACCGCATCTTCTCCCGAGCC 1192
QY 904 TTCTACACAGCAGGATACGGCTACAGATGTCTGCGTATCTACTGAAGCGGACAGCGC 963
Db 1193 TTCTACACAGCAGGATACGGCTACAGATGTCTGCGTATCTACTGAAGCGGACAGCGC 1252
QY 964 ACCGGCGAGGAACACACCTGTCCCTCTTTTGTGGTATGAAGGGCCCGGAATGACGCC 1023
Db 1253 ACCGGCGAGGAACACACCTGTCCCTCTTTTGTGGTATGAAGGGCCCGGAATGACGCC 1312
QY 1024 CTGCTGCGGTGGCCCTTCAACAGAGGTGACCTTAATGCTGCTCGACAGAAATACCGG 1083
Db 1313 CTGCTGCGGTGGCCCTTCAACAGAGGTGACCTTAATGCTGCTCGACAGAAATACCGG 1372
QY 1084 GAGCAGTGATGACGCTTACGGCCGACGCTGACTTCACTCTCTTTTTCAGAGGCGCAGTC 1143
Db 1373 GAGCAGTGATGACGCTTACGGCCGACGCTGACTTCACTCTCTTTTTCAGAGGCGCAGTC 1432
QY 1144 AAGCATGAAACATGCAAGCGGCTGCCCCCTCTTCTGCCCCGTCTCAAGATGAGGCA 1203
Db 1433 AAGCATGAAACATGCAAGCGGCTGCCCCCTCTTCTGCCCCGTCTCAAGATGAGGCA 1492
QY 1204 AAGAAATTCCTAGTGGGGACGATGCATCTTCAATCAAGGCGCATGTTGAGCCTGACAGG 1263
Db 1493 AAGAAATTCCTAGTGGGGACGATGCATCTTCAATCAAGGCGCATGTTGAGCCTGACAGG 1552
QY 1264 CTCTAA 1269
Db 1553 CTCTAA 1558

RESULT 7
BD276254
LOCUS
DEFINITION
VARIANTS OF TRAF2 WHICH ACT AS AN INHIBITOR OF TNF-ALPHA SIGNALING
PATHWAY.
ACCESSION
BD276254
VERSION
BD276254.1 GI:33086022
KEYWORDS
JP 2002542826-A/2.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1011)
```

```
AUTHORS Ivashchenko,Y.D., Iii,G.H.S., Pagnoni,M.F., Guo,X. and Clark,K.L.
TITLE VARIANTS OF TRAF2 WHICH ACT AS AN INHIBITOR OF TNF-ALPHA SIGNALING
JOURNAL PATHWAY
COMMENT Patent: JP 2002542826-A 2 17-DEC-2002;
Avantis Pharmaceuticals Products Inc,George H Searfoss III, Marco F
Pagnoni,Yuri D Ivashchenko,Kun Guo,Kenneth L Clark
OS Homo sapiens
PN JP 2002542826-A/2
PD 17-DEC-2002
PF 06-APR-2000 JP 2000615761
PR 30-APR-1999 US 60/131940
PI yuri d ivashchenko,george h searfoss iii,marco f pagnoni,kun
PI guo,
PI kenneth l clark
CC
FEATURES
source
FH Key Location/Qualifiers.
1..1011
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 79.4%; Score 1008; DB 6; Length 1011;
Best Local Similarity 100.0%; Pred. No. 1 6e-199;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 262 AGTTTCGGCCCTTCCAGATAATGTGCCCCGAGGAGGTGAGAGCCCTGCGGCGGTCTGT 321
Db 4 AGTTTCGGCCCTTCCAGATAATGTGCCCCGAGGAGGTGAGAGCCCTGCGGCGGTCTGT 63
QY 322 CCCAGTCATGATGCACCTGMAAGGGGACCTTGAAGAANTACGAGTTTCAGGACCCAGTC 381
Db 64 CCCAGTCATGATGCACCTGMAAGGGGACCTTGAAGAANTACGAGTTTCAGGACCCAGTC 123
QY 382 AAGACTTGTGGCAAGTCTCGAGTCCCTTGAGAGATTCACGCCCATCGGCTGCCTGAGAGC 441
Db 124 AAGACTTGTGGCAAGTCTCGAGTCCCTTGAGAGATTCACGCCCATCGGCTGCCTGAGAGC 183
QY 442 GTAGAGGGTGAGAAACAGCAGGACGACAGGTGCGTGGGTGCGGGAGCAGCTGGCCATG 501
Db 184 GTAGAGGGTGAGAAACAGCAGGACGACAGGTGCGTGGGTGCGGGAGCAGCTGGCCATG 243
QY 502 CTACTGAGCTCGGTGCTGGAGGCAAGCCCTCTTTGGAGACCAAGCCCAAGCGGGGTGCA 561
Db 244 CTACTGAGCTCGGTGCTGGAGGCAAGCCCTCTTTGGAGACCAAGCGGGGTGCA 303
QY 562 GAGCTCTGCAAGGTCGAGAGCTTGGAAGAACGCGCCACTTTTGAAGAACATTGTC 621
Db 304 GAGCTCTGCAAGGTCGAGAGCTTGGAAGAACGCGCCACTTTTGAAGAACATTGTC 363
QY 622 TGCGTCTGTAACCGGGAGGTGGAGAGGTGCGCATGACTGCCGAGGCTGCAGCCGCGAG 681
Db 364 TGCGTCTGTAACCGGGAGGTGGAGAGGTGCGCATGACTGCCGAGGCTGCAGCCGCGAG 423
QY 682 CACCGGCTGGAACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCAAGCAGCTGGAGAGG 741
Db 424 CACCGGCTGGAACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCAAGCAGCTGGAGAGG 483
QY 742 AGCATTCGCTCAAGGACCTGGCGATGGCTGACTTGGAGCAGAGGCTTTGGAGATGGAG 801
Db 484 AGCATTCGCTCAAGGACCTGGCGATGGCTGACTTGGAGCAGAGGCTTTGGAGATGGAG 543
QY 802 GCATCCACCTACGATGGGTCTTTCATCTGGAAGATCTCAGACTTCGCCAGGAAGCTCCAG 861
Db 544 GCATCCACCTACGATGGGTCTTTCATCTGGAAGATCTCAGACTTCGCCAGGAAGCTCCAG 603
QY 862 GAAGCTGTGGCTGGCCGCATACCGGCCATCTTCTCCAGCCTTCTACACGAGAGTAC 921
Db 604 GAAGCTGTGGCTGGCCGCATACCGGCCATCTTCTCCAGCCTTCTACACGAGAGTAC 663
QY 922 GGCTACAGAGATGTGCTCGGTATCTACTGAAGCGGACCGGACCGGCGGAGGAACACAC 981
```

664	Db	GGGTACAAGATGTGTCTGCGTATCTACCTTGAAACGGGACGGCACCGGGCGAGGAACACAC	723
982	QY	CTGTGCCCTCTCTTTTGTGGTGATGAAGGGCCCGAAATGACGCCCTGTGTGGGTGGCCCTTC	1041
724	Db	CTGTGCCCTCTCTTTTGTGGTGATGAAGGGCCCGAAATGACGCCCTGTGTGGGTGGCCCTTC	783
1042	QY	AACCAGAAGGTGACCTTAAATGCTGCTGCACAGAAATAACCGGAGACACGTGATTTAGCGCC	1101
784	Db	AACCAGAAGGTGACCTTAAATGCTGCTGCACAGAAATAACCGGAGACACGTGATTTAGCGCC	843
1102	QY	TTCAGGCGCCACGTGACTTTCATCTCTTTTTCAGAGGCCAGTCAACGACATGAACATCGCA	1161
844	Db	TTCAGGCGCCACGTGACTTTCATCTCTTTTTCAGAGGCCAGTCAACGACATGAACATCGCA	903
1162	QY	AGCGGTGCGCCCTCTCTCTGCCCCGCTTCCAAAGATGGAGGACAAAGAAATTCCTACGTGCGG	1221
904	Db	AGCGGTGCGCCCTCTCTCTGCCCCGCTTCCAAAGATGGAGGACAAAGAAATTCCTACGTGCGG	963
1222	QY	GACGATGCCATCTTCATCAAGGCCATTGTGGACTCGACAGGGCTCTAA	1269
964	Db	GACGATGCCATCTTCATCAAGGCCATTGTGGACTCGACAGGGCTCTAA	1011
RESULT 8			
BD224867	LOCUS	2262 bp DNA linear PAT 17-JUL-2003	
DEFINITION		Antisense modulation of expression of tumor necrosis factor receptor-associated factor (TRAF).	
ACCESSION		BD224867	
VERSION		BD224867.1 GI:33034637	
KEYWORDS		JP 2002526095-A/2.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		Baker,B.F., Cowsett,L.M., Monia,B.P. and Xu,X.S.	
TITLE		Antisense modulation of expression of tumor necrosis factor receptor-associated factor (TRAF)	
JOURNAL		Patent: JP 2002526095-A 2 20-AUG-2002;	
COMMENT		ISIS PHARMACEUTICALS INC. OS Homo sapiens (human) EN JP 2002526095-A/2 PD 20-AUG-2002 PF 05-OCT-1999 JP 2000574546 PI 06-OCT-1998 US 09/167109 PT BRENDA F BAKER, LEX M COWSETT, BRETT P MONIA, XIAOXING S XU PC C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC Antisense modulation of expression of tumor necrosis factor CC Antisense-associated factor (TRAF) FH Key Location/Qualifiers FT CDS (55)..(1560).	
FEATURES			
source		1..2262 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	
ORIGIN			
Query Match		75.6%; Score 959.6; DB 6; Length 2262;	
Best Local Similarity		81.7%; Pred. No. 1.8e-189;	
Matches 1230; Conservative		0; Mismatches 39; Indels 237; Gaps 1;	
QY	1	ATGCGTGCAGCTAGCGTGACCCCCCTGGCTCCCTGGAGTTGTACAGCCGCGCTTCTCC	60
Db	55	ATGCGTGCAGCTAGCGTGACCCCCCTGGCTCCCTGGAGTTGTACAGCCGCGCTTCTCC	114
QY	61	AGACCCCTCTGGGGACCAAGCTGGAGCAAGTACTGTGCTCCGCTGCAGAAAGTC	120
Db	115	AGACCCCTCTGGGGACCAAGCTGGAGCAAGTACTGTGCTCCGCTGCAGAAAGTC	174
QY	121	CTCCGACGGCCCTTCCAGGCGCAGTGGGCACCGGTACTGTCTCTCTGCTGGCCAGC	180


```

Db 1255 ACCGGGCGAGGAACACACCTGTCCTCTTTTGTGTGTATGAAGGGCCGGAATGACGCC 1314
Qy 1024 CTGTCGGTGGCCCTTCAACAGAAAGTGACCTTAATGTCTGCTCGACCAAGATAACCGG 1083
Db 1315 CTGTCGGTGGCCCTTCAACAGAAAGTGACCTTAATGTCTGCTCGACCAAGATAACCGG 1374
Qy 1084 GAGCAGTGATGAGCCCTTCAGGCCCGACGCTGACTCATCTCTTTTCAGAGCCAGTC 1143
Db 1375 GAGCAGTGATGAGCCCTTCAGGCCCGACGCTGACTCATCTCTTTTCAGAGCCAGTC 1434
Qy 1144 AACGACATGAACATCGCAAGCGGTGCCCCCTCTTCTGCCCCGCTCCCAAGATGGAGCCA 1203
Db 1435 AACGACATGAACATCGCAAGCGGTGCCCCCTCTTCTGCCCCGCTCCCAAGATGGAGCCA 1494
Qy 1204 AAGAAATTCCTACGTGCGGAGCATGCCATCTTATCAAGGCCATGTGACCTGACAGGG 1263
Db 1495 AAGAAATTCCTACGTGCGGAGCATGCCATCTTATCAAGGCCATGTGACCTGACAGGG 1554
Qy 1264 CTCTAA 1269
Db 1555 CTCTAA 1560

RESULT 10
AR211089
LOCUS AR211089 2262 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 2 from patent US 6399297.
ACCESSION AR211089
VERSION AR211089.1 GI:21514318
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2262)
AUTHORS Baker,B.F., Cowser,L.M., Monia,B.P. and Xu,X.S.
TITLE Antisense modulation of expression of tumor necrosis factor
receptor-associated factors (TRAFs)
JOURNAL Patent: US 6399297-A 2 04-JUN-2002;
FEATURES Location/Qualifiers
source 1..2262
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 75.6%; Score 959.6; DB 6; Length 2262;
Best Local Similarity 81.7%; Pred. No. 1.8e-189;
Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;

Qy 1 ATGGCTGAGCTAGCTGACCCGCCCTGGCTCCCTGGAGTTGCTACGCCGCGCTTCTCC 60
Db 55 ATGGCTGAGCTAGCTGACCCGCCCTGGCTCCCTGGAGTTGCTACGCCGCGCTTCTCC 114
Qy 61 AAGACCTCTCTGGGGAACAAAGCTGGAAGCAAGTACCTGTCTCCGCTGCGAGAAACGTC 120
Db 115 AAGACCTCTCTGGGGAACAAAGCTGGAAGCAAGTACCTGTCTCCGCTGCGAGAAACGTC 174
Qy 121 CTCGGAGGCCCTTCCAGGCGAGTGTTGGCCACGGTACTGCTCTCTTCTGCTGGCCAGC 180
Db 175 CTCGGAGGCCCTTCCAGGCGAGTGTTGGCCACGGTACTGCTCTCTTCTGCTGGCCAGC 234
Qy 181 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGTCTTCCAGGCGCATATATGAAGAA 240
Db 235 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGTCTTCCAGGCGCATATATGAAGAA 294
Qy 241 GGCAATTTCTATTTAGAAAGCAGTTCCGCTTCCAGATAATCTCCCGCAGGGAGGTG 300
Db 295 GGCAATTTCTATTTAGAAAGCAGTTCCGCTTCCAGATAATCTCCCGCAGGGAGGTG 354
Qy 301 GAGACCTCGCGCGCTCTGCTCCAGTGTGATGATGCACTTGGAGGGGACCTTGAAGAA 360
Db 355 GAGACCTCGCGCGCTCTGCTCCAGTGTGATGATGCACTTGGAGGGGACCTTGAAGAA 414
Qy 361 TACG----- 364

```

```

|||||
415 TACGAGAGTGCCACGAAGCGCGCTGCCGCTCATGTGACCGAATGTCCCGCGTGTAAA 474
365 ----- 364
475 GGCCTGTGTCGGCTTGGTGAAGAGGAGCGCCACCTGGAGACGAGTGCCCGGAGNAGAAGC 534
365 ----- 364
535 CTGAGCTCGCGCATTTGCCGGGACCCCTGCTCGGAGCAGACGTGAAGCGCAGCCACGAG 594
365 ----- 364
595 GTCTGCCCCAAGTTCCTTAACTTGTGACGCGTCCGGCAAGAAAGATCCCCGGGAG 654
365 -AGTTTCAGGACCAAGCTCAAGACTTGTGGCAAGTGTGAGTCCCTTGCAGATTCCAGGCC 423
655 AAGTTTCAGGACCAAGCTCAAGACTTGTGGCAAGTGTGAGTCCCTTGCAGATTCCAGGCC 714
424 ATCGGCTGCTCGACGCGTAGAGGGTGAGAAACAGCAGGAGCAGGAGTGCAGTGGCTG 483
715 ATCGGCTGCTCGACGCGTAGAGGGTGAGAAACAGCAGGAGCAGGAGTGCAGTGGCTG 774
484 CGGAGACACCTGGCCATGCTACTGAGCTCGGTGCTGGAGGCAAGAGCCCTCTTGGGAGAC 543
775 CGGAGACACCTGGCCATGCTACTGAGCTCGGTGCTGGAGGCAAGAGCCCTCTTGGGAGAC 834
544 CAGACCAAGCGGGGTGAGAGCTCTGAGAGGTGCGAGAGCTTGGAGAAAGAACGCGCC 603
835 CAGAGCCAAGCGGGGTGAGAGCTCTGAGAGGTGCGAGAGCTTGGAGAAAGAACGCGCC 894
604 ACTTTTGAGAACATTTGCTGCTGCTGAAACCGGAGGTGGAGAGGGTGGCCATGACTGCC 663
895 ACTTTTGAGAACATTTGCTGCTGCTGAAACCGGAGGTGGAGAGGGTGGCCATGACTGCC 954
664 GAGGCTCTGAGCGCGGACGACCGGCTGGACCAAGATGGAAGCCCTGAGTAGCAAG 723
955 GAGGCTCTGAGCGCGGACGCGCTGGACCAAGATGGAAGCCCTGAGTAGCAAG 1014
724 GTGAGCAGCTGGAGAGGAGCATTTGGCTCAAGCAACCTGGCGATGGCTGACTTGGAGCAG 783
1015 GTGAGCAGCTGGAGAGGAGCATTTGGCTCAAGCAACCTGGCGATGGCTGACTTGGAGCAG 1074
784 AAGGTCTTGGAGATGGAGGACATCCACCTAGATGGGTCTTTCATCTGGAAGATCTAGAC 843
1075 AAGGTCAAGGCTTCCAGGCGCAGTGTGGCCACCGGTACTGCTCTTCTGCTGCCAGC 1134
844 TTCGCCAGGAAGCTCCAGGAAGCTGTGGCTGGCGCATACCGGCATCTTCTCCGAGCC 903
1135 ATCTCTCAGAAAGCTCCAGGAAGCTGTGGCTGGCGCATACCGGCATCTTCTCCGAGCC 1194
904 TTCTACACAGCAGGTACGGCTACAAGATGTGTCTGGGTATCTACCTGAAACGCGAGCGC 963
1195 TTCTACACAGCAGGTACGGCTACAAGATGTGTCTGGGTATCTACCTGAAACGCGAGCGC 1254
964 ACCGGCGAGAGAAACACACTGTCCCTCTTCTTGTGTGTATGAAGGGCCCGAATGAGGCC 1023
1255 ACCGGCGAGAGAAACACACTGTCCCTCTTCTTGTGTGTATGAAGGGCCCGAATGAGGCC 1314
1024 CTGCTCGGTGGCCCTTCAACAGAAAGTGAACCTTAATGTGCTCGACCAAGATAACCGG 1083
1315 CTGCTCGGTGGCCCTTCAACAGAAAGTGAACCTTAATGTGCTCGACCAAGATAACCGG 1374
1084 GAGCAGTGATGAGCCCTTCAGGCCCGACGCTGACTCATCTCTTTTCAGAGCCAGTC 1143
1375 GAGCAGTGATGAGCCCTTCAGGCCCGACGCTGACTCATCTCTTTTCAGAGCCAGTC 1434
1144 AACGACATGAACATCGCAAGCGGTGCCCCCTCTTCTGCCCCGCTCCCAAGATGGAGCCA 1203
1435 AACGACATGAACATCGCAAGCGGTGCCCCCTCTTCTGCCCCGCTCCCAAGATGGAGCCA 1494
1204 AAGAAATTCCTACGTGCGGAGCATGCCATCTTATCAAGGCCATGTGACCTGACAGGG 1263

```


VERSION	AX335498.1	GI:18126217
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Young, P.B., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.	
TITLE	Cancer gene determination and therapeutic screening using signature gene sets	
JOURNAL	Patent: WO 0194629-A 6007 13-DEC-2001;	
FEATURES	Avalon Pharmaceuticals (US)	
source	Location/Qualifiers	
	1..2262	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
ORIGIN		
Query Match	75.6%	Score 959.6; DB 6; Length 2262;
Best Local Similarity	81.7%	Pred. No. 1.8e-189;
Matches 1230; Conservative	0; Mismatches 39; Indels 237; Gaps 1;	
QY	1	ATGGCTGCAGCTAGCGTAGACCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTCTCTCC 60
Db	55	ATGGCTGCAGCTAGCGTAGACCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTCTCTCC 114
QY	61	AAGACCTCTCTGGGACCAAGCTGGAAGCAAGTACTGTGTCTCGCTCGCGAAGACGTC 120
Db	115	AAGACCTCTCTGGGACCAAGCTGGAAGCAAGTACTGTGTCTCGCTCGCGAAGACGTC 174
QY	121	CTCCGAGGCCCTTCACAGGCGAGTGTGGCCACCGGTACTGTCTCTTCGCTTGGCCAGC 180
Db	175	CTCCGAGGCCCTTCACAGGCGAGTGTGGCCACCGGTACTGTCTCTTCGCTTGGCCAGC 234
QY	181	ATCCTCAGCTCTGGGCTCAGAACTGTGTGCTGTGTTCACAGGGCATATATGAAGAA 240
Db	235	ATCCTCAGCTCTGGGCTCAGAACTGTGTGCTGTGTTCACAGGGCATATATGAAGAA 294
QY	241	GGCATTTCTATTTAGAAAGCAGTTCCGCTTCCAGATAATGCTGCCGCGAGGAGGTG 300
Db	295	GGCATTTCTATTTAGAAAGCAGTTCCGCTTCCAGATAATGCTGCCGCGAGGAGGTG 354
QY	301	GAGAGCTCTCGGCCGTCTGTCTCCAGTGTGGATGCACCTGGAAGGGGACCTTGAAAGAA 360
Db	355	GAGAGCTCTCGGCCGTCTGTCTCCAGTGTGGATGCACCTGGAAGGGGACCTTGAAAGAA 414
QY	361	TACG-----364
Db	415	TACGAGAGTGCACGAGAGCGCGCTGCCGCTCATGCTGACCGAATGTCCCGGTGTAAA 474
QY	365	-----364
Db	475	GGCTTGGTCCGCTTGGTGAAAGGAGCGCCACCTGGAGCAGAGTGCCTGGAGAGACG 534
QY	365	-----364
Db	535	CTGAGCTCGCGCAATTGCGGGCACCTCTGCTGGAGCAGACGTGAAAGGCGCACCGAG 594
QY	365	-----364
Db	595	GTCTGCCCAAGTTCCCTTTAACTTGTGACGGCTGGGCAAGAAAGATCCCCGGGAG 654
QY	365	-AGTTTCAGGACCACTGTAAGACTTGTGGCAAGTGTGAGTCCCTTTGAGATTCACGCC 423
Db	655	AAAGTTTCAGGACCACTGTAAGACTTGTGGCAAGTGTGAGTCCCTTTGAGATTCACGCC 714
QY	424	ATCGGCTGCTCTGAGACGGTACGAGGTGAGAAACAGCAGGAGCAAGAGTGCAGTGGCTG 483
Db	715	ATCGGCTGCTCTGAGACGGTACGAGGTGAGAAACAGCAGGAGCAAGAGTGCAGTGGCTG 774
QY	484	CGGAGACACCTGGCCATGCTACTGAGCTCGGTGCTGGAGGCAAGACCCCTCTTTGGAGAC 543

MEDLINE 95366958
PUBMED 7639698
REFERENCE 2 (bases 655 to 1560)
AUTHORS Rothe,M., Wong,S.C., Henzel,W.J. and Goeddel,D.V.
TITLE A novel family of putative signal transducers associated with the
cytoplasmic domain of the 75 kDa tumor necrosis factor receptor
JOURNAL Cell 78 (4), 681-692 (1994)
MEDLINE 94349371
PUBMED 8069916
REFERENCE 3 (bases 1 to 2262)
AUTHORS Song,H.Y.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1994) Ho Y. Song, Physiology and Walther Oncology
Center, Indiana University School of Medicine, 975 W. Walnut St.,
Indianapolis, IN 46202, USA
COMMENT On Sep 6, 1995 this sequence version replaced gi:695148.
FEATURES
source
1..2262
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HeLa S3"
1..2262
/gene="TRAP3"
55..1560
/gene="TRAP3"
/note="TNF type 2 receptor binding protein"
/codon_start=1
/evidence=experimental
/product="tumor necrosis factor type 2 receptor associated
protein 3"
/protein_id="AA887706.1"
/db_xref="GI:975273"
translation="MAAASVTPPGSLELLQPGFSKTLTGKLEAKVLCASCRNVLRPP
FAQCHRVCSFLAILSSGPONCAACVHEGIYEGISILESSAFDPNARREVES
LPVCPDSCTWKGTILKYESCHGRCPMLITECPACKGLVRLGKXERHLEHCEPERS
LSCHRAPCCGADVAHVEVCPKPLTCDGGKKKIPEKFDHVKTCGKRVPCRF
HAIGLETVKQOEHEVQVREHLAMLLSVLEAKPLLDQSHVAGSELQRCBSLE
KKTAPENTVCLNREVERVAMTAACSRQRLDQDKIEALSKVQQLERSTIGLKDLA
MADLEQKVPQAQCCGRVCSFLASILRLQEAAGVAGRIPAIFSPAFVTSRYKMWCL
RVYNGDGRGTHLSLFPVMKMGNDALLRPENQKVTMLLDONNREHVIDAFRPD
VTSSEFPQVPNDMTASGCLPCVPKMEAKNSYVRDDAIFKAIVDLTGL"
misc_feature
154..330
/gene="TRAP3"
/note="encodes ring finger motif"
misc_feature
445..819
/gene="TRAP3"
/note="cysteine-histidine rich region"
misc_feature
679..723
/gene="TRAP3"
/note="encodes zinc finger-like motif"
misc_feature
928..1680
/gene="TRAP3"
/note="encodes TRAF domain"
/citation=[2]
ORIGIN
Query Match 75.6%; Score 959.6; DB 9; Length 2262;
Best Local Similarity 81.7%; Pred. No. 1.8e-189;
Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;
QY 1 ATGGCTGCAGTAGCTGACCCCTGGCTCCCTGGAGTTGCTACAGCCCGCTTCCTCC 60
DB 55 ATGGCTGCAGTAGCTGACCCCTGGCTCCCTGGAGTTGCTACAGCCCGCTTCCTCC 114
QY 61 AAGACCTCTCTGGGGACCAAGCTGGAGGCAAGTACCTGTGCTCCGCTTCGAGAACGTC 120
DB 115 AAGACCTCTCTGGGGACCAAGCTGGAGGCAAGTACCTGTGCTCCGCTTCGAGAACGTC 174
QY 121 CTCCGAGGCGCTTCAGGCGGAGTGTGGCCACCGGTACTGCTCTCTGCTGGCCAGC 180
DB 175 CTCCGAGGCGCTTCAGGCGGAGTGTGGCCACCGGTACTGCTCTCTGCTGGCCAGC 234

QY 181 ATCTCAGCTCTGGGCTCAGAACTGCTGCTGCTGCTTCAAGAGGGCATATATGAGAA 240
DB 235 ATCTCAGCTCTGGGCTCAGAACTGCTGCTGCTTCAAGAGGGCATATATGAGAA 294
QY 241 GGCATTTCTATTTTAAAGACAGTTCCGCTCTCCACAGATAATGCTCCCGCAGGAGGTG 300
DB 295 GGCATTTCTATTTTAAAGACAGTTCCGCTCTCCACAGATAATGCTCCCGCAGGAGGTG 354
QY 301 GAGAGCTCGCGGCTCTGCTCCAGTATGATGACCTTGGAGAGGGGACCTTGAAGAA 360
DB 355 GAGAGCTCGCGGCTCTGCTCCAGTATGATGACCTTGGAGAGGGGACCTTGAAGAA 414
QY 361 TACG----- 364
DB 415 TACAGAGCTGCCACGAGGCGCTGCTGCTGACCGAATGCTCCGCGGTGTAAA 474
QY 365 ----- 364
DB 475 GGCCTGCTCGGCTTGGTGAAGAGGAGCGCACCTGTGAGCAGCTGCCCGGAGAGAGC 534
QY 365 ----- 364
DB 535 CTGAGCTGCCGCGCATTTCCGCGGACACCTGCTGCGGAGCAGACGTGAAGGCGCACCGAG 594
QY 365 ----- 364
DB 595 GTCTGCCCCAAGTTCCCTTAACTTGTGACGGCTGCGGCAAGAAAGATCCCCCGGAG 654
QY 365 -AGTTTCAGGACCACTCAAGACTTGTGGCAAGTGTGAGTCCCTTGCAGATTCACGCC 423
DB 655 AAGTTTCAGGACCACTCAAGACTTGTGGCAAGTGTGAGTCCCTTGCAGATTCACGCC 714
QY 424 ATCGGCTGCTCGAGAGCGGTAGAGGGTGAGAAAACAGCAGGACGACGAGGTGCACTGGCTG 483
DB 715 ATCGGCTGCTCGAGAGCGGTAGAGGGTGAGAAAACAGCAGGACGACGAGGTGCACTGGCTG 774
QY 484 CGGAGACACTTGGCATGCTACTGAGTCTCGGTGCTGAGGCAAGCCCTCTTTGGGAGAC 543
DB 775 CGGAGACACTTGGCATGCTACTGAGTCTCGGTGCTGAGGCAAGCCCTCTTTGGGAGAC 834
QY 544 CAGAGCCACGCGGGGTGAGAGTCTCTCAGAGGTGCGAGAGCTTGGAGAGAGAGAGAGCGCC 603
DB 835 CAGAGCCACGCGGGGTGAGAGTCTCTCAGAGGTGCGAGAGCTTGGAGAGAGAGAGAGCGCC 894
QY 604 ACTTTTCAGAACATTTGCTGCTGCTCTGAACCGGAGGTGAGAGAGGTGGCCATGACTGCC 663
DB 895 ACTTTTCAGAACATTTGCTGCTGCTCTGAACCGGAGGTGAGAGAGGTGGCCATGACTGCC 954
QY 664 GAGGCTTGCAGCGCGGACGACCGGCTGGACCAAGACAGATTGAAAGCCCTGAGTAGCAAG 723
DB 955 GAGGCTTGCAGCGCGGACGACCGGCTGGACCAAGACAGATTGAAAGCCCTGAGTAGCAAG 1014
QY 724 GTGCAGCAGCTGGAGAGAGCATTGGGCTCAAGGACCTGGCGATGGCTGACTTTGGAGCAG 783
DB 1015 GTGCAGCAGCTGGAGAGAGCATTGGGCTCAAGGACCTGGCGATGGCTGACTTTGGAGCAG 1074
QY 784 AAGTCTTTGAGATGGAGGGCATCCACTAGATGGGGTCTTCACTGCGAAGATCTCAGAC 843
DB 1075 AAGTCTGAGGCTTCCAGGGCGAGTGTGGCCACCGTACTGCTCTCTGCTGCGCCAGC 1134
QY 844 TTCCGCGAGGAGCTCCAGGAGCTGTGGCTGGCGCGCATACCGCATCTTCTCCCGCAGCC 903
DB 1135 ATCTTCAGGAAGCTTCAGGAAGCTGTGGCTGGCGCGCATACCGCATCTTCTCCCGCAGCC 1194
QY 904 TTCTACACCGACAGGTACGGCTACCAAGATGTGTGCGTATCTACCTGAACGGCGAGCGG 963
DB 1195 TTCTACACCGACAGGTACGGCTACCAAGATGTGTGCGTATCTACCTGAACGGCGAGCGG 1254
QY 964 ACCGGCGAGGAAACACCTGCTCTCTTTGTTGTTGATGAGGGCCGGAATGAGCGC 1023
DB 1255 ACCGGCGAGGAAACACCTGCTCTCTTTGTTGTTGATGAGGGCCGGAATGAGCGC 1314
QY 1024 CTGCTGCGGTGGCCCTTCAACCAAGAGGTGACCTTAAATGCTGCTCGACCAAGATAACCGG 1083

LOCUS	AK054686	2094 bp	mRNA	linear	PRI 30-JAN-2004
DEFINITION	Homo sapiens cDNA FLJ30124 f1s, clone BRACE100093, highly similar to TNF RECEPTOR ASSOCIATED FACTOR 2.				
ACCESSION	AK054686				
VERSION	AK054686.1 GI:16549280				
KEYWORDS	Oligo capping; f1s (full insert sequence).				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oabayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwavanagi, T., Watanabe, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, S., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotaka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Theraishina, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hiki, T., Kobatake, N., Inaguchi, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakat, K., Iada, T., Nakamura, Y., Ohara, O., Isogai, T., and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs Nat. Genet. 36 (1), 40-45 (2004)				
TITLE	14702039				
JOURNAL	2				
PUBMED	Nishi, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project Unpublished				
REFERENCE	3 (bases 1 to 2094)				
AUTHORS	Isogai, T., Otsuki, T. and Sugiyama, T.				
TITLE	Direct Submission				
JOURNAL	Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.				
FEATURES	Location/Qualifiers				
source	1. .2094				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clones="BRACE100093"				
	/tissue_type="cerebellum"				
	/clone_lib="BRACE1"				
	/note="Cloning vector: pME18SFL3"				
	45. .1388				
	/note="unnamed protein product"				
	/codon_start=1				
	/protein_id="BAB70792.1"				
	/db_xref="GI:16549281"				
	/translation="MAAASVTPPGSLLELQPGFSKTLTGLKLEAKYLCACRNVLRRP				
	FOACGHRYCSFCUASILSSGPQNAACVHEGYIEGSILESSAFDPAARREVES				
	LPVAGDGGTGTGKLEKYEVPQACQMTFAVGRPRSPSPSYDVLVHPTGTGA				
	CLMSVEBETLLEHSCHEGCPMLTECPAGKGLRGLGERLHEHCKVQRLSCRC				
	RAPCCGADVKAHEVSCPKPLTCDGCGCKXIIPREKFOQDKIALSSKVQRLSRL				
	KDLAVALEQVLEMEASTVDYFVWIKISDFARKQEAAGRIPATISPAFYTRYGV				
	KMCRLIYNGDGTGRGTHLSLFFVWGPNDALLRWFNFQKVTMLLDQNNREHVIDA				
	FRPVTSSSPRPVNDNNIASGCLFPCFVSKMEAKNSYVRDDAIFIKAVDLITGL"				
ORIGIN	67.4%; Score 855.6; DB 9; Length 2094;				
	Query Match				
	Best Local Similarity 81.5%; Pred. No. 8.3e-168;				
	Matches 1095; Conservative 0; Mismatches 174; Indels 75; Gaps 6;				
Qy	1	ATGSGTCGAGCTAGCGTGACCCCTCGCTCCCTCGAGTTGCTACAGCCGGCTTCCTCC	60		
Db	45	ATGSGTCGAGCTAGCGTGACCCCTCGCTCCCTCGAGTTGCTACAGCCGGCTTCCTCC	104		
Qy	61	AAGACCCCTCTCTGGGAGCAAGCTGGAAGCAAGTACCTGTCTCCGCTGCAGAAAGCTC	120		
Db	105	AAGACCCCTCTCTGGGAGCAAGCTGGAAGCAAGTACCTGTCTCCGCTGCAGAAAGCTC	164		
Qy	121	CTCCGAGGCGCTTCCAGGGCGAGTGGGCGACCGGTACTGCTCTTCTGCTGGCCGAGC	180		
Db	165	CTCCGAGGCGCTTCCAGGGCGAGTGGGCGACCGGTACTGCTCTTCTGCTGGCCGAGC	224		
Qy	181	ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGTCTCAGAGGSCATATATGAAGAA	240		
Db	225	ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGTCTCAGAGGSCATATATGAAGAA	284		
Qy	241	GGCATTCTATTTTGAAGAACGATTCGGCTTCCAGATAATGCTGCCCGCAGGAGGTG	300		
Db	285	GGCATTCTATTTTGAAGAACGATTCGGCTTCCAGATAATGCTGCCCGCAGGAGGTG	344		
Qy	301	GAGAGCTCTGGGCGCTGTCTCCAGTGTGATGATGACCTTGGAGGGGACCTTGAAGAA	360		
Db	345	GAGAGCTCTGGGCGCTGTCTCCAGTGTGATGATGACCTTGGAGGGGACCTTGAAGAA	404		
Qy	361	TACGAGTTTCA-----GGACCACGTCAGAGCTTGTGGCAAGTGTGAGTCCCTT	409		
Db	405	TACGAGTTTCA-----GGACCACGTCAGAGCTTGTGGCAAGTGTGAGTCCCTT	464		
Qy	410	GCAGATTCCAC-----GGACCACGTCAGAGCTTGTGGCAAGTGTGAGTCCCTT	429		
Db	465	CCACGCTCTCCCAAGCAGTATGACCTTGTCTCTGACAGCTTCTCACTGGGGGTGAAGCC	524		
Qy	430	TGCTCTGAGACGGTGTAGAGGGTGTAGAAACACAG-----GAGCAGAGTGTGAGTCCGCTG	484		
Db	525	TGCTCTGAGTGTGTGGAGGAGAGACCGAGCTGCTCTTGAAGCTCCACGAGGCGCC	584		
Qy	485	GGGAGCAGCTGGGCGATCTACTGAGTGTGGTGTGGAGGCAAGGCC--CTCTTTGGGAGAC	543		
Db	585	TGCCCGCTCATGCTGACCGAATGTCCCGCTGCAAGAGCCCTGGTCCGCTTGGTGAAG	644		
Qy	544	CAGAGCCACCGGGGTGAGAGCTCTGTCAGAGGTGGAGAGCTGGAGAGAGACGGCC	603		
Db	645	GAGCGCACCTGGAGACGAGTGTCCCGGAGAGAGCTTGAGCTGCGGCAATGCGCGGCA	704		
Qy	604	ACTTTTGAGAACATTTGTCTGCTCTGTAACCGGGAGGTGGA---GAGGGTGGCCATGACT	660		
Db	705	CCCTGTCTGGGAGCAGACGTGAAGGGCGCACACGAGGTCTGCCCCCAAGTTCCCTTA	764		
Qy	561	GCCGAGCGCTTCAG-----CCGCGAGCAGCGCTTGGCCCAAGACAGATT	705		

Db	765	TGTGACGGCTCGGCAAGAAAGATCCCGGAGAAAGTTTCAGGACCAAGACAGATT	824
Qy	706	GAAGCCCTGAGTAGCAAGGTGACAGAGCTGGAGAGGAGCATTTGGCCCTCAAGGACCTTGGCG	765
Db	825	GAAGCCCTGAGTAGCAAGGTGACAGAGCTGGAGAGGAGCATTTGGCCCTCAAGGACCTTGGCG	884
Qy	766	ATGGCTGACTTGGAGGCAAGAGTCTTGGAGATGGAGGATCCACCTACGATGGGTCTTC	825
Db	885	ATGGCTGACTTGGAGGCAAGAGTCTTGGAGATGGAGGATCCACCTACGATGGGTCTTC	944
Qy	826	ATCTGGAAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGTGGCTGGCCCGCATACCC	885
Db	945	ATCTGGAAGATCTCAGACTTCGCCAGGAAGCTGTGGCTGGCCCGCATACCC	1004
Qy	886	GCCATCTTCTCCCGAGCTTCTACACGAGAGGTACGGCTACAAGATGTGTCTGCGGTATC	945
Db	1005	GCCATCTTCTCCCGAGCTTCTACACGAGAGGTACGGCTACAAGATGTGTCTGCGGTATC	1064
Qy	946	TACCTGAACGGCGACGGCACCGGGGAGGAACACACCTGTCCCTCTTCTTTTGTGGTGATG	1005
Db	1065	TACCTGAACGGCGACGGCACCGGGGAGGAACACACCTGTCCCTCTTCTTTTGTGGTGATG	1124
Qy	1006	AAGGCCCGGAATGACGCCCTCTGCGGTGGCCCTTCAACAGAGAGTGACCTTAATGCTG	1065
Db	1125	AAGGCCCGGAATGACGCCCTCTGCGGTGGCCCTTCAACAGAGAGTGACCTTAATGCTG	1184
Qy	1066	CTCGACCAAGATTAACGGGAGCAGTGATTGACGCTTTCAGGCCCGGACGTGCTTCATCC	1125
Db	1185	CTCGACCAAGATTAACGGGAGCAGTGATTGACGCTTTCAGGCCCGGACGTGCTTCATCC	1244
Qy	1126	TCTTTTCAGAGGCCAGTCAACGACATGAACATCGCAAGCGGCTGCCCTCTTCTGCCCC	1185
Db	1245	TCTTTTCAGAGGCCAGTCAACGACATGAACATCGCAAGCGGCTGCCCTCTTCTGCCCC	1304
Qy	1186	GTCCTCAAGATGGAGGCAAGAAATTCCTACGTGGGAGCATGCCATCTTTCATCAAGGCC	1245
Db	1305	GTCCTCAAGATGGAGGCAAGAAATTCCTACGTGGGAGCATGCCATCTTTCATCAAGGCC	1364
Qy	1246	ATTGTGACCTGACAGGGCTCTAA	1269
Db	1365	ATTGTGACCTGACAGGGCTCTAA	1388

Search completed: November 6, 2004, 20:48:51
Job time : 5538 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 16:50:28 ; Search time 676 Seconds
(without alignments)
9854.313 Million cell updates/sec

Title: US-10-018-030B-1
Perfect score: 1269
Sequence: 1 atggctgcagctagctgac.....tggacctgacagggctctaa 1269

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1269	100.0	2025	5	AAD01947 Human TRA
2	1008	79.4	1011	5	AAD01948 Human TRA
3	959.6	75.6	1506	10	ACF04633 TRAF2 pro
4	959.6	75.6	1506	12	ADM45823 TNF-alpha
5	959.6	75.6	2262	3	AAA55491 Human TRA
6	959.6	75.6	2262	5	AAD01949 Human TNF
7	959.6	75.6	2262	6	ABL65876 Lung carc
8	959.6	75.6	2262	6	ABL67670 Oesophagu
9	959.6	75.6	2262	8	ACD13346 Human DNA
10	959.6	75.6	2262	9	ADB80997 RING-SH c
11	855.6	67.4	2094	10	ADA52495 Human cod
12	701	55.2	2121	6	AB199821 Mouse lsc
13	699.4	55.1	2121	2	AAT12262 Mouse TRA
14	582.2	45.9	979	8	ACA57328 Human adi
15	296.6	23.4	2380	2	AAT31374 Epstein-B
16	296.6	23.4	2380	3	AAA55490 Human TEA
17	296.6	23.4	2380	6	ABK84255 Human CDN
18	296.6	23.4	2380	10	ADF76475 Novel hum
19	296.6	23.4	5981	8	ABX63823 Human MP2
20	295	23.2	2412	12	ADL22895 Human MP2
21	295	23.2	2412	12	ADL82946 Human PRO

ALIGNMENTS

RESULT 1

AAD01947

ID AAD01947 standard; cDNA; 2025 BP.

XX AAD01947;

AC AAD01947;

XX 26-MAR-2001 (first entry)

XX Human TRAF2 splice variant TRAF2TR (TRAF2 truncated) cDNA.

XX Human: tumour necrosis factor; TNF; TRAF2-FL; inhibitor; treatment;

XX TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;

XX anti-inflammatory; cardiac; myocardial infarction; splice variant;

XX vasotrophic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;

XX rheumatoid arthritis; immunosuppressive; Crohn's disease; psoriasis;

XX non-insulin dependent diabetes; inflammatory bowel disease; stroke;

XX neurodegenerative disease; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 55..1323

XX /*tag= a

XX /product= "TRAF2TR protein"

XX /note= "This region is specifically claimed in claim 1"

XX WO2000066737-A1.

XX 09-NOV-2000.

XX 06-APR-2000; 2000WO-US009178.

XX 30-APR-1999; 99US-0131940P.

XX (AVET) AVENTIS PHARM PROD INC.

XX Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;

XX WPI; 2001-007223/01.

XX P-PSDB; AAY1901.

XX New nucleic acid encoding variants of tumor necrosis factor receptor

XX associated factors useful for inhibiting tumor necrosis factor alpha-

PT regulated pathways, and for treating Crohn's disease, psoriasis, and
 PF rheumatoid arthritis.
 XX Claim 1; Fig 4a; 74pp; English.
 XX The present sequence is a cDNA encoding tumour necrosis factor (TNF)-
 CC receptor associated factor-truncated protein (TRAF2TR) which is a splice
 CC variant of human TRAF2 protein. TRAF2TR has an ability to inhibit TNF
 CC alpha signalling pathways. The TRAF2TR variant is useful for inhibiting
 CC diseases involving overproduction of TNFalpha, TNFalpha pathologies
 CC involving hyperactivation of nuclear factor kappa B (NFkB). The variant
 CC is also useful for inhibiting and treating inflammatory processes
 CC involving TNFalpha such as Crohn's disease, psoriasis, rheumatoid
 CC arthritis, graft versus host disease, non-insulin dependent diabetes,
 CC inflammatory bowel disease, and neurodegenerative diseases or
 CC cardiovascular disease such as cardiac ischaemia-reperfusion injury
 CC following myocardial infarction, coronary artery bypass surgery, cardiac
 CC transplantation or ischaemia-reperfusion injury in the central nervous
 CC system (CNS) following stroke, the progression and rupture of advanced
 CC coronary atherosclerotic plaques, development and progression of
 CC congestive heart failure, endothelial cell injury following balloon
 CC angioplasty, or apoptotic cell death of myocardial cells
 XX
 SQ Sequence 2025 BP; 408 A; 580 C; 650 G; 387 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1269; DB 5; Length 2025;
 Best Local Similarity 100.0%; Pred. No. 6.8e-275;
 Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ATGCTGAGTACGAGTACCGCCCGCTGGCTCCCTGAGTGTGTACAGCCGCGCTCTCC 60
 55 ATGCTGAGTACGAGTACCGCCCGCTGGCTCCCTGAGTGTGTACAGCCGCGCTCTCC 114
 61 AAGACCTCTCTGGGGAACCAAGCTGGAAGCCCAAGTACCTGTCTCCGCTTCAGAAACGTC 120
 115 AAGACCTCTCTGGGGAACCAAGCTGGAAGCCCAAGTACCTGTCTCCGCTTCAGAAACGTC 174
 121 CTCGCGAGCCCTTCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTCTCTCTCTCTCTCT 180
 175 CTCGCGAGCCCTTCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTCTCTCTCTCTCTCT 234
 181 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 235 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 294
 241 GGCATTTCTATTTTAAAGCAGTTCGCGCTTCCAGATATATGCTGCTGCTGCTGCTGCTGCTG 300
 295 GGCATTTCTATTTTAAAGCAGTTCGCGCTTCCAGATATATGCTGCTGCTGCTGCTGCTGCTG 354
 301 GAGAGCTGCGCGCGCTGTGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 360
 355 GAGAGCTGCGCGCGCTGTGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 414
 361 TACGAGTTTCAGGACCCAGCTCAAGACTTGTGGCAAGTGTGAGTCCCTTTCAGATTTCCAC 420
 415 TACGAGTTTCAGGACCCAGCTCAAGACTTGTGGCAAGTGTGAGTCCCTTTCAGATTTCCAC 474
 421 GGCATTCGCTCTCTGAGACCGGTAGAGGTGAGAAACAGCAGGAGCAGAGGTGCAGTGG 480
 475 GGCATTCGCTCTCTGAGACCGGTAGAGGTGAGAAACAGCAGGAGCAGAGGTGCAGTGG 534
 481 CTGCGGAGACACCTGGCCATCTACTAGCTGCGGTGTGAGGCAAGCCCTCTTGGGA 540
 535 CTGCGGAGACACCTGGCCATCTACTAGCTGCGGTGTGAGGCAAGCCCTCTTGGGA 594
 541 GACGAGACCCACCGCGGTGAGAGCTCTCTGAGAGGTGCGAGAGCTTGGAGAGAGACG 600
 595 GACGAGACCCACCGCGGTGAGAGCTCTCTGAGAGGTGCGAGAGCTTGGAGAGAGACG 654
 601 GCCACTTTTGAGAACTTGTCTGGTCTGAGTAAACCGGAGGTGAGAGGTGGCCATGACT 660
 655 GCCACTTTTGAGAACTTGTCTGGTCTGAGTAAACCGGAGGTGAGAGGTGGCCATGACT 714

661 GCCGAGGCTGCTGAGCCGCGCAGCACCGGCTGGACCAAGACAGATTGAAGCCCTGAGTAGC 720
 715 GCCGAGGCTGCTGAGCCGCGCAGCACCGGCTGGACCAAGACAGATTGAAGCCCTGAGTAGC 774
 721 AAGGTGACGAGCTGGAGAGGAGGAGCATTTGGCCCTCAAGACCTGGCGATGGCTGACTTGGAG 780
 775 AAGGTGACGAGCTGGAGAGGAGGAGCATTTGGCCCTCAAGACCTGGCGATGGCTGACTTGGAG 834
 781 CAGAAAGGTCTTGGAGATGGAGGAGCATTCACCTACGATGGGTCTTTCATCTGGAAGATCTCA 840
 835 CAGAAAGGTCTTGGAGATGGAGGAGCATTCACCTACGATGGGTCTTTCATCTGGAAGATCTCA 894
 841 GACTTTCGCGAGAAAGCTCCAGAAAGCTGTGGCTGGCGCATACCCGCGCATTTCTCCCCA 900
 895 GACTTTCGCGAGAAAGCTCCAGAAAGCTGTGGCTGGCGCATACCCGCGCATTTCTCCCCA 954
 901 GCCTTCTACACCGAGGTACGGCTACAAGATGTCTGCGTATCTACCTGAACGGGAC 960
 955 GCCTTCTACACCGAGGTACGGCTACAAGATGTCTGCGTATCTACCTGAACGGGAC 1014
 961 GGCACCGGCGCAGGAACACACCTGTCTCTCTTCTTGTGGTGTGAAGGGCCGAAATGAC 1020
 1015 GGCACCGGCGCAGGAACACACCTGTCTCTCTTCTTGTGGTGTGAAGGGCCGAAATGAC 1074
 1021 GCCTTCTGCTGCGGTGGCCCTTCAACCGAGAGGTGACCTTAATGCTGCTCGACCAAGTAAC 1080
 1075 GCCTTCTGCTGCGGTGGCCCTTCAACCGAGAGGTGACCTTAATGCTGCTCGACCAAGTAAC 1134
 1081 CGGAGACGCTGATTGACGCTTTCAGGCGCCGACGTGACTTCATCTCTTTTTCAGAGGCCA 1140
 1135 CGGAGACGCTGATTGACGCTTTCAGGCGCCGACGTGACTTCATCTCTTTTTCAGAGGCCA 1194
 1141 GTCAACGACATGAACATCGAAGCGGCTGCCCTCTTCTGCGCGCTCTCAAGATGGAG 1200
 1195 GTCAACGACATGAACATCGAAGCGGCTGCCCTCTTCTGCGCGCTCTCAAGATGGAG 1254
 1201 GCAGAGAAATTCCTACGCTGCGGAGCGATGCCATCTTCATCAAGGCGCATGTGGACCTGACA 1260
 1255 GCAGAGAAATTCCTACGCTGCGGAGCGATGCCATCTTCATCAAGGCGCATGTGGACCTGACA 1314
 1261 GGGCTCTAA 1269
 1315 GGGCTCTAA 1323
 RESULT 2
 AAD01948
 ID AAD01948 standard; cDNA; 1011 BP.
 XX
 AC AAD01948;
 XX
 DT 26-MAR-2001 (first entry)
 XX
 DE Human TRAF2TR variant, TRAF2 truncated-deleted (TRAF2TD) cDNA.
 XX
 DE Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
 KW TNF-receptor associated factor; TRAF2 truncated-deleted; TRAF2TD;
 KW anti-inflammatory; cardiant; mutant; muten; myocardial infarction;
 KW vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
 KW antiatherosclerotic; immunosuppressive; Crohn's disease; psoriasis;
 KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;
 KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
 KW neurodegenerative disease; variant; TRAF2 truncated; TRAF2TR; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH 1..1011
 FT CDS /*tag= a
 FT /product= "TRAF2TD protein"
 XX
 PN W0200066737-A1.

XX 09-NOV-2000.
XX 06-APR-2000; 2000WO-US009178.
XX 30-APR-1999; 99US-0131940P.
XX (AVET) AVENTIS PHARM PROD INC.
XX Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
XX WPI; 2001-007223/01.
XX P-PSDB; AAY71902.
XX New nucleic acid encoding variants of tumor necrosis factor receptor
XX associated factors useful for inhibiting tumor necrosis factor alpha-
XX regulated pathways, and for treating Crohn's disease, psoriasis, and
XX rheumatoid arthritis.
XX Claim 2; Fig 3a; 74pp; English.
XX The present sequence is a cDNA encoding tumour necrosis factor (TNF)-
XX receptor associated factor truncated-deleted (TRAF2ND) protein which is a
XX variant of human TRAF2R (truncated). This sequence includes both the
XX naturally occurring splice variation and a deletion at the 5' end of
XX human TRAF2-FL (full-length) nucleic acid sequence. TRAF2ND has an
XX ability to inhibit TNF alpha signalling pathways. The TRAF2ND variant is
XX useful for inhibiting diseases involving over production of TNFalpha, B
XX TNFalpha pathologies involving hyperactivation of nuclear factor kappa B
XX (NFkB). The variant is also useful for inhibiting and treating
XX inflammatory processes involving TNFalpha such as Crohn's disease,
XX psoriasis, rheumatoid arthritis, graft versus host disease, non-insulin
XX dependent diabetes, inflammatory bowel disease, and neurodegenerative
XX diseases or cardiovascular disease such as cardiac ischaemia-reperfusion
XX injury following myocardial infarction, coronary artery bypass surgery,
XX cardiac transplantation or ischaemia-reperfusion injury in the central
XX nervous system (CNS) following stroke, the progression and rupture of
XX advanced coronary atherosclerotic plaques, development and progression of
XX congestive heart failure, endothelial cell injury following balloon
XX angioplasty, or apoptotic cell death of myocardial cells
XX
XX Sequence 1011 BP; 226 A; 282 C; 315 G; 188 T; 0 U; 0 Other;
Query Match 79.4%; Score 1008; DB 5; Length 1011;
Best Local Similarity 100.0%; Pred. No. 2.2e-216;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 262 AGTTGGCCCTCCAGATAATGCTGCCGACGAGGAGGTGGAGGCTGCGCGGCTCTGT 321
DB 4 AGTTGGCCCTCCAGATAATGCTGCCGACGAGGAGGTGGAGGCTGCGCGGCTCTGT 63
QY 322 CCCAGTGATGATGCACCTGGAAGGGGACCCCTGAAAGAAATACAGTTTCAGGACCACTC 381
DB 64 CCCAGTGATGATGCACCTGGAAGGGGACCCCTGAAAGAAATACAGTTTCAGGACCACTC 123
QY 382 AGACTTGGCAAGTGTGAGTCCCTTGCAGATCCAGCCATCGGCTGCTCGAGACG 441
DB 124 AGACTTGGCAAGTGTGAGTCCCTTGCAGATCCAGCCATCGGCTGCTCGAGACG 183
QY 442 GTAGAGGGTGAGAAACAGCAGGAGCAGCAGGTGTCAGTGGCTCGGAGCACCCTGGCCATG 501
DB 184 GTAGAGGGTGAGAAACAGCAGGAGCAGCAGGTGTCAGTGGCTCGGAGCACCCTGGCCATG 243
QY 502 CTACTGAGTCCGGTGTGAGGCAAGCCCTCTTTGGGAGACACAGGACCGGGGTCA 561
DB 244 CTACTGAGTCCGGTGTGAGGCAAGCCCTCTTTGGGAGACACAGGACCGGGGTCA 303
QY 562 GAGCTCTCCAGAGGTGCGAGAGCTGGAGAGAGAGAGCGCCACTTTTGAACAATTGTC 621
DB 304 GAGCTCTCCAGAGGTGCGAGAGCTGGAGAGAGAGAGCGCCACTTTTGAACAATTGTC 363
QY 622 TCGCTCTGAAACCGGAGGTGGAGAGGTGGCCATCACTGCCAGGCTCGAGCGCGGAG 681

DB 364 TGGTCTCTGAACCCGGGAGGTGGAGAGGGTGCCATGACTGCCGAGGCTGCGAGCGGAG 423
QY 682 CACCGGCTGGACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCGAGCAGCTGGAGAGG 741
DB 424 CACCGGCTGGACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCGAGCAGCTGGAGAGG 483
QY 742 AGCATTGGCCTCAAGGACCTGGCGATGGCTGACTTTGGAGCAAGAGGTCTTGGAGATGGAG 801
DB 484 AGCATTGGCCTCAAGGACCTGGCGATGGCTGACTTTGGAGCAAGAGGTCTTGGAGATGGAG 543
QY 802 GCATCCACCTACGATGGGCTCTTTCATCTGGAAGATCTCAGACTTTCGCCAGCAAGCTCCAG 861
DB 544 GCATCCACCTACGATGGGCTCTTTCATCTGGAAGATCTCAGACTTTCGCCAGCAAGCTCCAG 603
QY 862 GAAGCTGTGGTGGCGCGCATACCGCGCATCTTCTCCAGCCTTTACACAGCAGGTAC 921
DB 604 GAAGCTGTGGTGGCGCGCATACCGCGCATCTTCTCCAGCCTTTACACAGCAGGTAC 663
QY 922 GGCTACAAGATGTCTGCGTATCTACCTGAACGGCGACGCGACCGGGCGAGGACACAC 981
DB 664 GGCTACAAGATGTCTGCGTATCTACCTGAACGGCGACGCGACCGGGCGAGGACACAC 723
QY 982 CTGTCCCTCTTCTTTGGTGAAGAGGCGCCGATGACCCCTGCTGCGGTGGCCCTTC 1041
DB 724 CTGTCCCTCTTCTTTGGTGAAGAGGCGCCGATGACCCCTGCTGCGGTGGCCCTTC 783
QY 1042 AACAGAGGAGTGAATTAAGTCTGCTGACCAAGATTAACGGGAGCAAGTGTGAGCGCC 1101
DB 784 AACAGAGGAGTGAATTAAGTCTGCTGACCAAGATTAACGGGAGCAAGTGTGAGCGCC 843
QY 1102 TTCAGGCGCCAGCTGACTTTCATCTCTTTTCAGAGGCGAGTCAACGACATGAACATCGCA 1161
DB 844 TTCAGGCGCCAGCTGACTTTCATCTCTTTTCAGAGGCGAGTCAACGACATGAACATCGCA 903
QY 1162 AGCGCTGCGCCCTCTTCTGCGCCGCTCTCAAGATGAGGCAAGAAATTCCTACGTCCGG 1221
DB 904 AGCGCTGCGCCCTCTTCTGCGCCGCTCTCAAGATGAGGCAAGAAATTCCTACGTCCGG 963
QY 1222 GACCATGCCATCTTTCATCAAGGCGCATTTGACCTGACAGGCTCTAA 1269
DB 964 GACCATGCCATCTTTCATCAAGGCGCATTTGACCTGACAGGCTCTAA 1011
RESULT 3
ACF04633
ID ACF04633 standard; DNA; 1506 BP.
XX ACF04633;
XX AC ACF04633;
XX DT 18-DEC-2003 (first entry)
XX TRAF2 protein coding sequence.
XX DE TRAF2; inflammatory response; rheumatoid arthritis; lTbetaR;
XX KW lymphocytin-beta receptor; modulator; cancer; immunological disease;
XX KW apoptosis; cytotoxic; immunosuppressive; antirheumatic; antiarthritic;
XX KW antiinflammatory; dermatological; nephrotropic; antithyroid;
XX KW thyromimetic; muscular-Gen; neuroprotective; antianaemic; haemostatic;
XX KW vasotropic; antidiabetic; gene; ds.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX CDS 1..1506
XX FT /*tag= a
XX FT /product= "TRAF2"
XX XN WO2003066834-A2.
XX XN 14-AUG-2003.
XX XN 10-FEB-2003; 2003WO-US003923.
XX XN

OR-FEB-2002; 2002US-0355183P.
 (AMHP) WYETH.
 Kuai J, Wooters JL, Nickbarg EB, Qiu Y, Lin L;
 WPI; 2003-748125/70.
 P-PSDB; ABR84599.
 New purified lymphotoxin-beta receptor protein complex, useful for
 identifying modulators of lymphotoxin-beta receptor activity or
 expression for treating or preventing cancer or an autoimmune disorder,
 e.g. vasculitis or diabetes.
 Disclosure; Page 6; Opp; English.
 The present invention relates to a purified complex comprising a
 lymphotoxin beta receptor (Lbetrar) polypeptide and Smac polypeptide. The
 lymphotoxin-beta receptor (Lbetrar) complex is useful for identifying
 modulators of Lbetrar activity or expression for treating or preventing
 cancer or an immune disorder such as autoimmune disorder, e.g. rheumatoid
 arthritis, systemic lupus erythematosus, Goodpasture's syndrome, Grave's
 disease, Hashimoto's thyroiditis, pemphigus vulgaris, myasthenia gravis,
 scleroderma, autoimmune haemolytic anaemia, autoimmune thrombocytopenic
 purpura, polymyositis, dermatomyositis, pernicious anaemia, Sjogren's
 syndrome, ankylosing spondylitis, vasculitis, or type I diabetes
 mellitus. The present sequence is the coding sequence of a TRAF2 protein,
 which forms part of the complex of the invention
 Sequence 1506 BP; 317 A; 453 C; 460 G; 276 T; 0 U; 0 Other;
 Query Match 75.6%; Score 959.6; DB 10; Length 1506;
 Best Local Similarity 81.7%; Pred. No. 1.7e-205;
 Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;
 QY 1 ATGCTCAGCTACGCTGACCCCTCCCTGGCTCCCTGGAGTTGTACAGCCCGCTTCTCC 60
 DB 1 ATGCTCAGCTACGCTGACCCCTCCCTGGCTCCCTGGAGTTGTACAGCCCGCTTCTCC 60
 QY 61 AAGACCTCTCTGGGGACCAAGCTGGAAAGCAAGTACCTGTCTCCGCTCGAGAAACGTC 120
 DB 61 AAGACCTCTCTGGGGACCAAGCTGGAAAGCAAGTACCTGTCTCCGCTCGAGAAACGTC 120
 QY 121 CTCGGAGGCTTCCAGGGCAGTGGCCACCGGTACTGCTCTCTCTGCTGCTGCTGCTG 180
 DB 121 CTCGGAGGCTTCCAGGGCAGTGGCCACCGGTACTGCTCTCTCTGCTGCTGCTGCTG 180
 QY 181 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 DB 181 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 QY 241 GGCAATTTCTATTAGAAAGCAGTTCGGCTTCCAGATATGCTGCTGCTGCTGCTGCTGCTG 300
 DB 241 GGCAATTTCTATTAGAAAGCAGTTCGGCTTCCAGATATGCTGCTGCTGCTGCTGCTGCTG 300
 QY 301 GAGAGCTTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 DB 301 GAGAGCTTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 361 TACG----- 364
 DB 361 TACGAGAGCTGCCACGAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 365 ----- 364
 DB 421 GGCTGGTCCGCTTGTGTAAAGAGGCGCCACCTGGAGCAGAGTCCCGGAGAGAGC 480
 QY 365 ----- 364
 DB 481 CTGAGCTCCGGCATTTGGCGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 365 ----- 364

DB 541 GTCTGCCCAAGTTCCCTTAACCTTGTGACGGCTGCGGCAAGAGAGATCCCGCGGAG 600
 QY 365 -AGTTTCAGGACACGCTCAAGACTTGTGGCAAGTGTGAGTCCCTTTCAGATTCACGCC 423
 DB 601 AAGTTTCAGGACACGCTCAAGACTTGTGGCAAGTGTGAGTCCCTTTCAGATTCACGCC 660
 QY 424 ATCGCTGCTCTCGAGACGGTAGAGGGTGAAGAAACAGCAGGAGACGAGGTGCTGCTG 483
 DB 661 ATCGCTGCTCTCGAGACGGTAGAGGGTGAAGAAACAGCAGGAGACGAGGTGCTGCTG 720
 QY 484 CGGAGACCTTGGCCATCTACTAGCTCGGTGCTGGAGCAAGAGCCCTTCTTGGAGAC 543
 DB 721 CGGAGACCTTGGCCATCTACTAGCTCGGTGCTGGAGCAAGAGCCCTTCTTGGAGAC 780
 QY 544 CAGAGCCACGCGGGGTGAGAGCTCTCTGAGAGGTGCGAGAGCTTGGAGAAAGACGCGCC 603
 DB 781 CAGAGCCACGCGGGGTGAGAGCTCTCTGAGAGGTGCGAGAGCTTGGAGAAAGACGCGCC 840
 QY 604 ACTTTTGAGAACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
 DB 841 ACTTTTGAGAACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 664 GAGGCTCTGAGCCGCGCAGCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
 DB 901 GAGGCTCTGAGCCGCGCAGCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 724 GTGAGCAGCTGAGAGAGAGCAATTTGGCTTCAAGACCTTGGAGGTGCTGCTGCTGCTGCTGCTG 783
 DB 961 GTGAGCAGCTGAGAGAGAGCAATTTGGCTTCAAGACCTTGGAGGTGCTGCTGCTGCTGCTGCTG 1020
 QY 784 AAGGCTTTGGAGATGGAGGATCCACCTACGATGGGCTTTCATCTGGAAGATCTCAGAC 843
 DB 1021 AAGGCTTTGGAGATGGAGGATCCACCTACGATGGGCTTTCATCTGGAAGATCTCAGAC 1080
 QY 844 TTCCGACAGAAAGCTTCCAGAAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903
 DB 1081 ATCTCTCAGAAAGCTTCCAGAAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 QY 904 TTCTACACAGCAGGTAGGCTCAAGATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 963
 DB 1141 TTCTACACAGCAGGTAGGCTCAAGATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
 QY 964 ACCGCGCAGGAAACACACCTCTCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1023
 DB 1201 ACCGCGCAGGAAACACACCTCTCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 QY 1024 CTGCTGCGGTGCTTCAACAGAGAGTGAACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1083
 DB 1261 CTGCTGCGGTGCTTCAACAGAGAGTGAACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 QY 1084 GAGCAGCTGATTGAGCGCTTCAAGCGCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1143
 DB 1321 GAGCAGCTGATTGAGCGCTTCAAGCGCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 QY 1144 AACGACATGAACATCGAAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1203
 DB 1381 AACGACATGAACATCGAAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 QY 1204 AAGATTCCTAGCTGCGGAGCGATCCCATCTTCATCAGAGGCTTGTGAGCTGACAGGG 1263
 DB 1441 AAGATTCCTAGCTGCGGAGCGATCCCATCTTCATCAGAGGCTTGTGAGCTGACAGGG 1500
 QY 1264 CTCTAA 1269
 DB 1501 CTCTAA 1506

RESULT 4
 ADM45823
 ID ADM45823 standard; cDNA; 1506 BP.
 XX
 AC
 AC
 XX
 ADM45823;

QY 1144 AACGACATGAACATCGCAAGCGGTGCCCCCTCTCTGCCCCCTCTCCCAAGATGGAGGCA 1203
 DB 1381 AACGACATGAACATCGCAAGCGGTGCCCCCTCTCTGCCCCCTCTCCCAAGATGGAGGCA 1440
 QY 1204 AAGAAATTCCTACGTCGCGGACGATGCCATCTTATCAAGGCCATTGGACCTGACAGGG 1263
 DB 1441 AAGAAATTCCTACGTCGCGGACGATGCCATCTTATCAAGGCCATTGGACCTGACAGGG 1500
 QY 1264 CTCTAA 1269
 DB 1501 CTCTAA 1506

RESULT 5
 ID AAA55491 standard; DNA; 2262 BP.
 AC AAA55491;
 XX 30-AUG-2000 (first entry)
 DE Human TRAF2 nucleotide sequence locus name HSU12597.
 XX Tumour necrosis factor receptor-associated factor; TRAF; human;
 KW anti-sense oligonucleotide; phosphorothioate; antiproliferative;
 KW anti-inflammatory; E-selectin; jun kinase; ds.
 XX Homo sapiens.
 OS
 PN WO200020435-A1.
 PD 13-APR-2000.
 PF 05-OCT-1999; 99WO-US023171.
 PR 06-OCT-1998; 98US-00167109.
 PA (ISIS-) ISIS PHARM INC.
 PI Baker BF, Cowsett LM, Monia BP, Xu XS;
 DR WPI; 2000-303732/26.
 PS P-PSDB; RAY98165.
 PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
 PT necrosis factor receptor-associated factor (TRAF), useful for treating
 PT diseases associated with TRAF expression such as inflammatory diseases.
 XX Example 16; Page 109-111; 170pp; English.

XX The present invention relates to antisense oligonucleotides (see AAA55496
 CC -A55757) which are targeted to nucleic acids encoding a human tumour
 CC necrosis factor receptor-associated factor (TRAF). The antisense
 CC sequences comprise at least one modified internucleotide linkage, which
 CC is a phosphorothioate linkage. The oligonucleotides also include at least
 CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
 CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
 CC TRAF1-6. Included in the invention is a method for treating a human
 CC having a disease associated with the expression of TRAF comprising
 CC administering an antisense oligonucleotide. The reduction of jun kinase
 CC activation in cells comprises contacting the cells with an antisense
 CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
 CC selectin expression in cells or tissues comprises contacting the cells or
 CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
 CC The antisense oligonucleotides have antiproliferative and anti-
 CC inflammatory activity and are useful for treating disorders associated
 CC with cell proliferation and inflammation. The antisense oligonucleotides
 CC may also be used as a diagnostic probe for studying gene function

Sequence 2262 BP; 452 A; 664 C; 727 G; 419 T; 0 U; 0 Other;
 Query Match 75.6%; Score 959.6; DB 3; Length 2262;

Best Local Similarity 81.7%; Pred. No. 1.9e-205;
 Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;

QY 1 ATGGCTGAGCTAGCTGACACCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC 60
 DB 55 ATGGCTGAGCTAGCTGACACCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC 114
 QY 61 AAGACCTCTCTGGGACCAAGCTGGAAGCAAGTACCTGTCTCCGCTCGAGAAAGTC 120
 DB 115 AAGACCTCTCTGGGACCAAGCTGGAAGCAAGTACCTGTCTCCGCTCGAGAAAGTC 174
 QY 121 CTCGCGAGCCCTTCCAGGCGCAGTGGCCACCGGTACTGCTCTCTGCTGCGCAGC 180
 DB 175 CTCGCGAGCCCTTCCAGGCGCAGTGGCCACCGGTACTGCTCTCTGCTGCGCAGC 234
 QY 181 ATCTCAGCTCTGGGCTCTGAACTGTGCTGCTGCTTTCAGAGGCGATATATGAAGAA 240
 DB 235 ATCTCAGCTCTGGGCTCTGAACTGTGCTGCTGCTTTCAGAGGCGATATATGAAGAA 294
 QY 241 GGCATTTCTATTTAGAAAGCAGTTCCGCTTCCAGATATGCTGCCCGCAGGAGTG 300
 DB 295 GGCATTTCTATTTAGAAAGCAGTTCCGCTTCCAGATATGCTGCCCGCAGGAGTG 354
 QY 301 GAGAGCTCTCCGCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 355 GAGAGCTCTCCGCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 414
 QY 361 TACG----- 364
 DB 415 TACGAGAGCTGCCAGAGGCGCTGCCCGCTCATGTGACCGAATGTCCCGCTGTAAA 474
 QY 365 ----- 364
 DB 475 GGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 534
 QY 365 ----- 364
 DB 535 CTGAGCTCTCCGCGCTATGCCGCGCACCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594
 QY 365 ----- 364
 DB 595 GTCTGCCCCAAGTTCCCTTAACTTTGTGACGGCTGCGGCAAGAGAGATCCCTCCGGAG 654
 QY 365 -AGTTTCAGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
 DB 655 AAGTTTCAGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714
 QY 424 ATCGGCTCTCTGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTG 483
 DB 715 ATCGGCTCTCTGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTG 774
 QY 484 CGGAGACCTCTGGCCATGCTACTGAGCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
 DB 775 CGGAGACCTCTGGCCATGCTACTGAGCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 834
 QY 544 CAGACCTCTGAGAGCTGAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
 DB 835 CAGACCTCTGAGAGCTGAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
 QY 604 ACTTTTGAGAACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
 DB 895 ACTTTTGAGAACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
 QY 664 GAGGCTCTGAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
 DB 955 GAGGCTCTGAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
 QY 724 GTGACGAGCTGAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
 DB 1015 GTGACGAGCTGAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
 QY 784 AAGGCTCTGAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843

Db 1075 AAGGTGAGCCCTTCCAGCGGAGTGTCGCCACCGTACTGCTCTTCTGCTGCGCCAGC 1134
 Qy 844 TTGCGCAGGAAGCTCCAGGAAGCTGTGGTGCGCCGATACCCGCCATCTTCTCCCGACCC 903
 Db 1135 ATCTCTCAGGAAGCTCCAGGAAGCTGTGGTGCGCCGATACCCGCCATCTTCTCCCGACCC 1194
 Qy 904 TTCTACACAGCAGGTACGGCTACAGATGTCTCTGCGTATCTACTGAGCGGACCGC 963
 Db 1195 TTCTACACAGCAGGTACGGCTACAGATGTCTCTGCGTATCTACTGAGCGGACCGC 1254
 Qy 964 ACCGGCGAGGAAACACCTGTCCCTCTTCTTTTGTGGTGATGAAGGGCCGGAATGACGCC 1023
 Db 1255 ACCGGCGAGGAAACACCTGTCCCTCTTCTTTTGTGGTGATGAAGGGCCGGAATGACGCC 1314
 Qy 1024 CTGCTCGGTGCGCCCTTCAACAGAGGTGACCTTAATGCTGCTGACAGATTAACCGG 1083
 Db 1315 CTGCTCGGTGCGCCCTTCAACAGAGGTGACCTTAATGCTGCTGACAGATTAACCGG 1374
 Qy 1084 GAGCAGCTGATTGAGCCCTTTCAGGCGCCGACGTGACTTCATCTCTTTTCAGAGGCGAGTC 1143
 Db 1375 GAGCAGCTGATTGAGCCCTTTCAGGCGCCGACGTGACTTCATCTCTTTTCAGAGGCGAGTC 1434
 Qy 1144 AACGACATGAACATCGCAAGCGGCTGCCCTCTCTCTGCGCGCTTCCAAAGATGAGGCA 1203
 Db 1435 AACGACATGAACATCGCAAGCGGCTGCCCTCTCTCTGCGCGCTTCCAAAGATGAGGCA 1494
 Qy 1204 AAGATTCTCTAGTGGCGGACGATGCCATCTTTCATCAAGGCCATGTGACCTGACAGGG 1263
 Db 1495 AAGATTCTCTAGTGGCGGACGATGCCATCTTTCATCAAGGCCATGTGACCTGACAGGG 1554
 Qy 1264 CTCTAA 1269
 Db 1555 CTCTAA 1560
 RESULT 6
 AD001949
 ID AAD01949 standard; cdNA; 2262 BP.
 XX
 AC AAD01949;
 DT
 DT 26-MAR-2001 (first entry)
 XX
 DE Human TNF-receptor associated factor (TRAF2) cDNA.
 XX
 KW Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
 KW TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
 KW TRAF2 truncated-deleted; TRAF2TD; antiinflammatory; cardiant; vasotropic;
 KW antipsoriatic; antineumatic; antiarthritic; antidiabetic;
 KW antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
 KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;
 KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
 KW neurodegenerative disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 55..1560
 FT /*tag= a
 FT /product= "Human TRAF2 protein"
 FT 58..315
 FT /*tag= b
 FT /note= "This region is truncated in TRAF2TD nucleic acid
 sequence"
 FT 421..657
 FT /*tag= c
 FT /note= "This region is truncated both in TRAF2TR and
 TRAF2TD nucleic acid sequences"
 XX
 WO200066737-A1.
 XX
 PD 09-NOV-2000.
 XX

PF 06-APR-2000; 2000WO-US009178.
 PR 30-APR-1999; 99US-0131940P.
 PA (AVET) AVENTIS PHARM PROD INC.
 XX
 PI Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
 XX
 XX WPI; 2001-007223/01.
 DR P-PSDB; AAY/1903.
 XX
 XX
 PT New nucleic acid encoding variants of tumor necrosis factor receptor
 PT associated factors useful for inhibiting tumor necrosis factor alpha-
 PT regulated pathways; and for treating Crohn's disease, psoriasis, and
 PT rheumatoid arthritis.
 XX
 XX Example 1; Fig 4a; 74pp; English.
 XX
 CC The present sequence is a cDNA encoding a full-length (i.e. non-spliced)
 CC form of human tumour necrosis factor (TNF)-receptor associated factor
 CC (TRAF2) protein (referred to in the specification as TRAF2-FL). TRAF2-FL
 CC has two variants, a splice variant of TRAF2 referred as "TRAF2 truncated"
 CC (TRAF2TR) and a TRAF2 expression construct with enhanced dominant
 CC negative properties referred as "TRAF2 truncated-deleted" (TRAF2TD).
 CC TRAF2-TR and TRAF2-TD are capable of inhibiting TNF alpha signalling
 CC pathways. TRAF2 variants are useful for inhibiting diseases involving
 CC over production of TNFalpha, TNFalpha pathologies involving
 CC hyperactivation of nuclear factor kappa B (NFkB). The variants are also
 CC useful for inhibiting and treating inflammatory processes involving
 CC TNFalpha such as Crohn's disease, psoriasis, rheumatoid arthritis, graft
 CC versus host disease, non-insulin dependent diabetes, inflammatory bowel
 CC disease, and neurodegenerative diseases or cardiovascular disease such as
 CC cardiac ischaemia-reperfusion injury following myocardial infarction.
 CC coronary artery bypass surgery, cardiac transplantation or ischaemia-
 CC reperfusion injury in the central nervous system (CNS) following stroke,
 CC the progression and rupture of advanced coronary atherosclerotic plaques,
 CC development and progression of congestive heart failure, endothelial cell
 CC injury following balloon angioplasty, or apoptotic cell death of
 CC myocardial cells
 XX
 SQ Sequence 2262 BP; 452 A; 664 C; 727 G; 419 T; 0 U; 0 Other;
 Query Match 75.6%; Score 959.6; DB 5; Length 2262;
 Best Local Similarity 81.7%; Pred. No. 1.9e-205;
 Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;
 Qy 1 ATGCTGCAGCTAGCTGACCCCTCCCTGGCTCCCTGGAGTTGCTAGACGCCGCTTCTCC 60
 Db 55 ATGCTGCAGCTAGCTGACCCCTCCCTGGCTCCCTGGAGTTGCTAGACGCCGCTTCTCC 114
 Qy 61 AAGACCTCTCTGGGGACCAAGCTGGAAGCCAAAGTACCTGTCTCCGCTGCAGAAAGCTC 120
 Db 115 AAGACCTCTCTGGGGACCAAGCTGGAAGCCAAAGTACCTGTCTCCGCTGCAGAAAGCTC 174
 Qy 121 CTCGGAGGCGCTTCCAGGCGGAGTGTGGCCACCGGTACTGCTCTCTGCTGGCGCAGC 180
 Db 175 CTCGGAGGCGCTTCCAGGCGGAGTGTGGCCACCGGTACTGCTCTCTGCTGGCGCAGC 234
 Qy 181 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGTGTTTACGAGGCGCATATATGAAGAA 240
 Db 235 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGTGTTTACGAGGCGCATATATGAAGAA 294
 Qy 241 GGCATTTCATTTTAGAAGCAGTTCGGCTTCCCGAGATAATCTGCTCCGCGAGGAGGTG 300
 Db 295 GGCATTTCATTTTAGAAGCAGTTCGGCTTCCCGAGATAATCTGCTCCGCGAGGAGGTG 354
 Qy 301 GAGAGCTCGCGCGCTGTCTGCTCCAGTGATGATGACCTTGAAGGGGACCCCTGAAGAA 360
 Db 355 GAGAGCTCGCGCGCTGTCTGCTCCAGTGATGATGACCTTGAAGGGGACCCCTGAAGAA 414
 Qy 361 TACG-----
 Db 415 TACGAGAGCTGCCACGAAGGCGCTGCCCGCTCATGCTGACCGAATGTCCTCCGCTGTAAA 474

QY 365 ----- 364
 Db 475 GGCCTGGTCCGCTTGGTAAAGAGGCGCCACCTGGAGCAGGAGTGGCCCGGAGAGAGC 534
 QY 365 ----- 364
 Db 535 CTGAGCTGCGGCGCATTTGCGGCGCACCTGCTGCGAGCAGACGTTGAAGGCGCACCCAGAG 594
 QY 365 ----- 364
 Db 595 GTCTGCCCAAGTTCCCTTTAACTTTGTGACGGCTGGCGCAAGAGAGATCCCCCGGGAG 654
 QY 365 -AGTTTCAGGACCAAGTCAAGACTTTGTGGCAAGTGTGAGTTCCTTTCAGATTCCAGCC 423
 Db 655 AAGTTTCAGGACCAAGTCAAGACTTTGTGGCAAGTGTGAGTTCCTTTCAGATTCCAGCC 714
 QY 424 ATCGCTGCTCGAGACGGTAGAGGTTGAGAAACAGCAGGAGCAGAGGTTGAGTGGCTG 493
 Db 715 ATCGCTGCTCGAGACGGTAGAGGTTGAGAAACAGCAGGAGCAGAGGTTGAGTGGCTG 774
 QY 484 CCGGAGCACCTGGCCATGCTACTGAGCTCGGTGCTGGAGGCAAGCCCTCTTTGGGAGAC 543
 Db 775 CCGGAGCACCTGGCCATGCTACTGAGCTCGGTGCTGGAGGCAAGCCCTCTTTGGGAGAC 834
 QY 544 CAGAGCCACGCGGGGTGAGAGCTCTGAGAGTGGAGAGCCTGGAGAAAGAGAGAGCGCC 603
 Db 835 CAGAGCCACGCGGGGTGAGAGCTCTGAGAGTGGAGAGCCTGGAGAAAGAGAGAGCGCC 894
 QY 604 ACTTTTGAGAACATTTGCTGGCTCTGAAACGCGAGGTGGAGGGTGGCCATGACTGCC 663
 Db 895 ACTTTTGAGAACATTTGCTGGCTCTGAAACGCGAGGTGGAGGGTGGCCATGACTGCC 954
 QY 664 GAGCCTGCAAGCCGCGAGCAACGCGCTCGAACAGAAAGATTGAAGCCCTGAGTAGCAAG 723
 Db 955 GAGCCTGCAAGCCGCGAGCAACGCGCTCGAACAGAAAGATTGAAGCCCTGAGTAGCAAG 1014
 QY 724 GTGAGAGCTGGAGAGGAGCATTTGGCTCAGAGACCTGGCGATGCTGACTTTGGAGCAG 783
 Db 1015 GTGAGAGCTGGAGAGGAGCATTTGGCTCAGAGACCTGGCGATGCTGACTTTGGAGCAG 1074
 QY 784 AAGTCTTTGAGAGTGGAGGATCCACCTAGCATGGGTCTTTCATCTGGAAGATCTCAGAC 843
 Db 1075 AAGTCTAGGCGCTTCCAGGCGCAGTGTGGCCACCGGTACTGCTCTTCTGCTGGCCAGC 1134
 QY 844 TTCCCGCAGGAGCTCCAGAGAGCTGTGGCTGGCGGATACCGCCATCTTCTCCCGAGCC 903
 Db 1135 ATCTCAGGAAGCTCCAGGAAGCTGTGGCTGGCGGATACCGCCATCTTCTCCCGAGCC 1194
 QY 904 TTCTACACCAAGAGTACGGGTACAGATGTGTCTGGGTATCTACCTGAACGCGGAGCGGC 963
 Db 1195 TTCTACACCAAGAGTACGGGTACAGATGTGTCTGGGTATCTACCTGAACGCGGAGCGGC 1254
 QY 964 ACCGGGCGAGAAACACCTGTCCCTTTCTTTGTGTGTGTGAAGAGGCGCCGAATGACGCC 1023
 Db 1255 ACCGGGCGAGAAACACCTGTCCCTTTCTTTGTGTGTGTGAAGAGGCGCCGAATGACGCC 1314
 QY 1024 CTGCTGCGGTGGCCCTTCAACAGAGGTGACCTTAATGCTGCTGACACAGAAATAACCGG 1083
 Db 1315 CTGCTGCGGTGGCCCTTCAACAGAGGTGACCTTAATGCTGCTGACACAGAAATAACCGG 1374
 QY 1084 GAGCAGGTGATGAGCCTTTAGGCGGCGGAGCTTTTCTGCGCCGCTTCCAGATGGAGGCA 1143
 Db 1375 GAGCAGGTGATGAGCCTTTAGGCGGCGGAGCTTTTCTGCGCCGCTTCCAGATGGAGGCA 1434
 QY 1144 AACACATGACATGCAAGGCGGTGGCCCTTCTTCTGCGCCGCTTCCAGATGGAGGCA 1203
 Db 1435 AACACATGACATGCAAGGCGGTGGCCCTTCTTCTGCGCCGCTTCCAGATGGAGGCA 1494
 QY 1204 AAGAAATCTACGTGCGGAGCAGTGGCCATCTTTCATCAAGGCCATTTGTGACCTGACAGGG 1263
 Db 1495 AAGAAATCTACGTGCGGAGCAGTGGCCATCTTTCATCAAGGCCATTTGTGACCTGACAGGG 1554

QY 1264 CTCTAA 1269
 Db 1555 CTCTAA 1560
 RESULT 7
 ID ABL65876
 XX ABL65876 standard; DNA; 2262 BP.
 AC ABL65876;
 XX DT 15-MAY-2002 (first entry)
 DE Lung cancer related gene sequence SEQ ID NO:4213.
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; Gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 OS Homo sapiens.
 XX WO200194629-A2.
 XX PD 13-DEC-2001.
 XX PF 30-MAY-2001; 2001WO-US010838.
 XX PR 05-JUN-2000; 2000US-0209473P.
 PR 05-JUN-2000; 2000US-0209531P.
 PR 18-SEP-2000; 2000US-0233133P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
 PR 20-SEP-2000; 2000US-0234052P.
 PR 22-SEP-2000; 2000US-0234509P.
 PR 22-SEP-2000; 2000US-0234567P.
 PR 25-SEP-2000; 2000US-0234923P.
 PR 25-SEP-2000; 2000US-0234924P.
 PR 25-SEP-2000; 2000US-0235077P.
 PR 25-SEP-2000; 2000US-0235082P.
 PR 25-SEP-2000; 2000US-0235134P.
 PR 25-SEP-2000; 2000US-0235280P.
 PR 26-SEP-2000; 2000US-0235637P.
 PR 26-SEP-2000; 2000US-0235638P.
 PR 27-SEP-2000; 2000US-0235711P.
 PR 27-SEP-2000; 2000US-0235720P.
 PR 27-SEP-2000; 2000US-0235840P.
 PR 27-SEP-2000; 2000US-0235863P.
 PR 28-SEP-2000; 2000US-0236028P.
 PR 28-SEP-2000; 2000US-0236032P.
 PR 28-SEP-2000; 2000US-0236033P.
 PR 28-SEP-2000; 2000US-0236034P.
 PR 28-SEP-2000; 2000US-0236109P.
 PR 28-SEP-2000; 2000US-0236111P.
 PR 29-SEP-2000; 2000US-0236842P.
 PR 29-SEP-2000; 2000US-0236891P.
 PR 02-OCT-2000; 2000US-0237172P.
 PR 02-OCT-2000; 2000US-0237173P.
 PR 02-OCT-2000; 2000US-0237278P.
 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237598P.
 PR 03-OCT-2000; 2000US-0237604P.
 PR 03-OCT-2000; 2000US-0237606P.
 PR 03-OCT-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.
 XX (AVAL-) AVALON PHARM.
 XX

Query Match	75.6%	Score 959.6	DB 9	Length 2262
Best Local Similarity	81.7%	Pred. No. 1.9e-205		
Matches 1230	Conservative 0	Mismatches 39	Indels 237	Gaps 1
Qy 1	ATGGCTGACGTAGCGTACGCCGCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC	60		
Db 55	ATGGCTGACGTAGCGTACGCCGCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC	114		
Qy 61	AAGACCCCTCTGGGACCAAGCTGGAAAGCCAAAGTACTGTGCTCCGCTCGAAGAGCTC	120		
Db 115	AAGACCCCTCTGGGACCAAGCTGGAAAGCCAAAGTACTGTGCTCCGCTCGAAGAGCTC	174		
Qy 121	CTCGCAGGCCCTTCAGAGCGCAGTGGCCACCGGTACTGCTCTCTCTCCCTGGCCAGC	180		
Db 175	CTCGCAGGCCCTTCAGAGCGCAGTGGCCACCGGTACTGCTCTCTCTCCCTGGCCAGC	234		
Qy 181	ATCCTCAGCTCTGGGCCCTCAGAACTGTGCTGCTGTGTTCCAGAGGCAATATATGAAGAA	240		
Db 235	ATCCTCAGCTCTGGGCCCTCAGAACTGTGCTGCTGTGTTCCAGAGGCAATATATGAAGAA	294		
Qy 241	GGCAATTTCTATTTAGAAAGCAAGTTCCGCTTCCAGATAATGCTGCCCGCAGGAGGTG	300		
Db 295	GGCAATTTCTATTTAGAAAGCAAGTTCCGCTTCCAGATAATGCTGCCCGCAGGAGGTG	354		
Qy 301	GAGAGCTGCTCGGCCGCTCTGTCCAGGTATGATGACACCTGGAAAGGGAACCTTGAAAGAA	360		
Db 355	GAGAGCTGCTCGGCCGCTCTGTCCAGGTATGATGACACCTGGAAAGGGAACCTTGAAAGAA	414		
Qy 361	TACG-----	364		
Db 415	TACGAGAGCTGCCACGAAGGCCGCTGCCGCTCATGTGACCGGAATGTCGCGGTGTAAA	474		
Qy 365	-----	364		
Db 475	GGCCTGCTCGCCTTGTGTGTAAGGAGGGCCACTGTGAGCAGCAGTGCCCGGAGAGNAGC	534		
Qy 365	-----	364		
Db 535	CTGAGCTCCGGCATTCGCCGGCACCCCTGCTCGGAGCAGACGTGAAGGGCGACCAAG	594		
Qy 365	-----	364		
Db 595	GTCTGCCCAAGTTCCCTTAACTTGTGAACGCTGCGGCAAGAAGAAGATCCCCCGGAG	654		
Qy 365	-AGTTTCAGGACCAAGTCAAGACTTGTGGCAAGTGTGAGTCCCTTGACATTCACGCC	423		
Db 655	AAGTTTCAGGACCAAGTCAAGACTTGTGGCAAGTGTGAGTCCCTTGACATTCACGCC	714		
Qy 424	ATCGCTGCTCGAGACGTTAGAGGTTGAGAAACAGCAGGAGCAGCAGGTGCACTGGCTG	483		
Db 715	ATCGCTGCTCGAGACGTTAGAGGTTGAGAAACAGCAGGAGCAGCAGGTGCACTGGCTG	774		
Qy 484	CGGAGACACCTGGCCATGCTACTCAGCTCGGTGCTGGAGGCAAAAGCCCTCTTGGGAGAC	543		
Db 775	CGGAGACACCTGGCCATGCTACTCAGCTCGGTGCTGGAGGCAAAAGCCCTCTTGGGAGAC	834		
Qy 544	CAGAGCCACGCGGGTTCAGACTCCTTCAGAGGTCGAGAGCCTTGAGAGAAAGACGCC	603		
Db 835	CAGAGCCACGCGGGTTCAGACTCCTTCAGAGGTCGAGAGCCTTGAGAGAAAGACGCC	894		
Qy 604	ACTTTTGAGAACATTGCTCGTGGTCTCTGAAACCGGAGGTGGAGAGGTTGGCCATCAGTCC	663		
Db 895	ACTTTTGAGAACATTGCTCGTGGTCTCTGAAACCGGAGGTGGAGAGGTTGGCCATCAGTCC	954		
Qy 654	GAGGCTTCGACCGGSCAGCACCGGCTGGACCAAGACAAAGATTGAAGGCCCTGAGTAGCAAG	723		
Db 955	GAGGCTTCGACCGGSCAGCACCGGCTGGACCAAGACAAAGATTGAAGGCCCTGAGTAGCAAG	1014		
Qy 724	GTGCAGCAGCTGGAGAGGACATTGGCCTTCAGGACCTGGCGATGGCTGACTTCGAGCAG	783		
Db 1015	GTGCAGCAGCTGGAGAGGACATTGGCCTTCAGGACCTGGCGATGGCTGACTTCGAGCAG	1074		
Qy 784	AAGGTCTTTGGAGATGGAGGCAATCCACCTACGATGGGGTCTTTCATCTGGAAGATCTCAGAC	843		

RESULT 11	
ADA52495	
ID	ADA52495 standard; cDNA; 2094 BP.
XX	
AC	ADA52495;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Human coding sequence, SEQ ID 63.
XX	
KW	Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW	Gene therapy; human; secretory protein; membrane proteins; cancer;
KW	inflammatory disease; osteoporosis; neurological disease; gene; ss.
XX	
CS	Homo sapiens.
XX	
FN	EPI293569-A2.
XX	
PD	19-MAR-2003.
XX	
PF	21-MAR-2002; 2002EP-00006586.
XX	
PR	14-SEP-2001; 2001JP-00328381.
PR	24-JAN-2002; 2002US-0350435P.
XX	
PA	(HELI-) HELIX RES INST.
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.
XX	
PI	Isoqai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI	Yanamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX	
DR	WPI; 2003-395539/38.
DR	P-PSDB; ADA54134.
XX	
PT	New polynucleotides encoding full-length polypeptides, e.g. secretory
PT	and/or membrane proteins, useful for developing medicines for diseases in

PT which the gene is involved, or as target molecules for gene therapy.
 XX Claim 1; SEQ ID NO 63; 205pp; English.

XX The present invention relates to novel human secretory or membrane
 CC proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS2433-
 CC ADAS4071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 2094 BP; 419 A; 610 C; 661 G; 404 T; 0 U; 0 Other;

Query Match 67.4%; Score 855.6; DB 10; Length 2094;
 Best Local Similarity 81.5%; Pred. NO. 4.1e-182;
 Matches 1095; Conservative 0; Mismatches 174; Indels 75; Gaps 6;

QY 1 ATGGCTGAGCTAGCGTACACCCCTCGCTCCCTGGAGTGTCTACAGCCCGGCTTCTCC 60
 DB 45 ATGGCTGAGCTAGCGTACACCCCTCGCTCCCTGGAGTGTCTACAGCCCGGCTTCTCC 104
 QY 61 AAGACCTCTCTGGGACCAAGCTGGAAGCCAAAGTACTGTCTCCGCTGCGAAGACGTC 120
 DB 105 AAGACCTCTCTGGGACCAAGCTGGAAGCCAAAGTACTGTCTCCGCTGCGAAGACGTC 164
 QY 121 CTCCGAGCCCTTCCAGCGCAGTGTGGCCACCGGTACTGCTCTCTGCTGCGCCAGC 180
 DB 165 CTCCGAGCCCTTCCAGCGCAGTGTGGCCACCGGTACTGCTCTCTGCTGCGCCAGC 224
 QY 181 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGTGTTCACGAGGCGATATGAAGAA 240
 DB 225 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGTGTTCACGAGGCGATATGAAGAA 284
 QY 241 GGCATTTCTATTAGAAAGCAGTTCGCTCCAGTATGCTGCTGCTGCTGCTGCTGCTG 300
 DB 285 GGCATTTCTATTAGAAAGCAGTTCGCTCCAGTATGCTGCTGCTGCTGCTGCTGCTG 344
 QY 301 GAGAGCTTCCGCGCTGTGCTCCAGTGTGATGTCACCTGGAAGGGGACCTCGAAAGAA 360
 DB 345 GAGAGCTTCCGCGCTGTGCTCCAGTGTGATGTCACCTGGAAGGGGACCTCGAAAGAA 404
 QY 361 TACGAGTTCA -----GACACAGCTCAAGACTGTGGCAAGTGTGAGTCTCCTT 409
 DB 405 TACGAGTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
 QY 410 GCAGATTCAC -----GCCATCGGC 429
 DB 465 CCAGCTTCCCAAGCAGTATGACCTTGTCTGTCAGCTTCTCTACTGGGCTGAAGCC 524
 QY 430 TGCCTCGAGACGGTGAAGGTTGAAGAACAGAG -----GAGCAGAGGTGCACTGCTGC 484
 DB 525 TGTCTGATGTGTGTGGAGGAGAGACGGAGCTGCTCTTGAAGCTGCCACGAAGGCCG 584
 QY 485 GGGAGCACCTGGCCATCTACTAGCTCGTGTGCTGGAGGCAAGCC -CCTCTTGGGAGAC 543
 DB 585 TGCCCGCTCATGCTGACCGATGTCCCGCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCT 644
 QY 544 CAGAGCCACCGGGTTCAGAGCTCTCTGAGAGTGGCGAGAGCTGAGAGAGAGAGAGCGCC 603
 DB 645 GAGCGCCACCTGGAGACGAGTGCCTGGAGAGAGAGCTGAGCTGCTGCTGCTGCTGCTGCT 704
 QY 604 ACTTTTGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 DB 705 CCTGTGCTGGAGCAGACGTGAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
 QY 661 GCGAGGCTCGAC -----CCGCGAGCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
 DB 765 TGTGACGCTGCGCAAGAGAGATCTCCCGGAGAGAGTTTTCAGACCAAGACAGATT 824
 QY 706 GAGACCTTGTAGTACAGTGTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765
 DB 825 GAAAGCCCTGAGTACAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 884
 QY 766 ATGGCTGACTTGGAGCAGAGAGTCTTGGAGATGGAGGATCCACCTACGATGGGCTCTTC 825

DB 885 ATGGCTGACTTGGAGCAGAGAGTCTTGGAGATGGAGGATCCACCTACGATGGGCTCTTC 944
 QY 826 ATCTGGAAGATCTCAGACTTCCCGAGGAGCTCCAGGAGAGCTGTGGCTGGCGCATACCC 885
 DB 945 ATCTGGAAGATCTCAGACTTCCCGAGGAGAGCTCCAGGAGAGCTGTGGCTGGCGCATACCC 1004
 QY 886 GGCATCTTCTCCCGAGCTTCTACACCGAGGAGTACGCTCAAGATGTGTGCTGCTGATC 945
 DB 1005 GGCATCTTCTCCCGAGCTTCTACACCGAGGAGTACGCTCAAGATGTGTGCTGCTGATC 1064
 QY 946 TACCTGAGCGGAGGAGGAGCCCGGGGAGGAGACACACCTGTCTCTCTTGTGTGATG 1005
 DB 1065 TACCTGAGCGGAGGAGGAGCCCGGGGAGGAGACACACCTGTCTCTCTTGTGTGATG 1124
 QY 1006 AAGGGCCCGAATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065
 DB 1125 AAGGGCCCGAATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1184
 QY 1066 CTGACCGAGATTAACCGGAGCAGCTGATTAACGCTTTCAGGCGGAGCTGACTTCATCC 1125
 DB 1185 CTGACCGAGATTAACCGGAGCAGCTGATTAACGCTTTCAGGCGGAGCTGACTTCATCC 1244
 QY 1126 TCTTTTCAGAGCCAGTCAACGAGCATGAACATGCAAGCGGCTGCTGCTGCTGCTGCTGCT 1185
 DB 1245 TCTTTTCAGAGCCAGTCAACGAGCATGAACATGCAAGCGGCTGCTGCTGCTGCTGCTGCT 1304
 QY 1186 GTCTCAAGATGGAGCAAGAAATTCCTACGCTGGGAGCGATGCTTCTTCATCAAGGCC 1245
 DB 1305 GTCTCAAGATGGAGCAAGAAATTCCTACGCTGGGAGCGATGCTTCTTCATCAAGGCC 1364
 QY 1246 ATTTGGACCTGACAGGCTCTAA 1269
 DB 1365 ATTTGGACCTGACAGGCTCTAA 1388

RESULT 12
 ABI99821
 ID ABI99821 standard; cDNA; 2121 BP.

XX AC ABI99821;
 XX DT 07-VAR-2002 (first entry)
 XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:935.
 DE Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
 XX Mus musculus.
 XX WO200188188-A2.
 XX 22-NOV-2001.
 XX 18-MAY-2001; 2001WO-JP004192.
 XX 18-MAY-2000; 2000JP-00145977.
 PA (UNYI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 DR WPI; 2002-034733/04.
 DR P-PSDB; ABB57335.
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 XX genes.
 PS Claim 2; Page 2360-2364; 2690pp; English.

CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99912 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention.

XX SQ Sequence 2121 BP; 507 A; 560 C; 615 G; 439 T; 0 U; 0 Other;
 Query Match 55.2%; Score 701; DB 6; Length 2121;
 Best Local Similarity 71.0%; Pred. No. 2e-147;
 Matches 1069; Conservative 0; Mismatches 200; Indels 237; Gaps 1;

QY 1 ATGGCTGACGTAGCTGACCCCTCCCTGCTCCCTGGAGTTGCTACAGCCCGCTTCTCC 60
 DB 48 ATGGCTGACGACGAGTGTGCTCCCTGCTCCCTAGAACTGCTACAGCTGCTTCTCC 107
 QY 61 AGACCCCTCTGGGGACCAAGCTGGAGCCAGTACCTGCTCCGCTCGAGAAACGTC 120
 DB 108 AGACCCCTCTGGGGACCAAGCTGGAGCCAGTACCTGCTCCGCTCGAGAAACATC 167
 QY 121 CTCGGAGGCGCTTCAGGCGCAGTGTGGCCACCGGTACTGCTCTTCTGCTGCCAGC 180
 DB 168 CTGCGGAGGCGCTTCAGGCGCAGTGTGGCCACCGGTACTGCTCTTCTGCTGCCAGC 227
 QY 181 ATCTCAGCTCTGGGCTCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 DB 228 ATCTCAGCTCTGGGCTCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 287
 QY 241 GGCATTCTCTATTAGAAAGCAGTGTGGGCTTCCAGATAAATGCTCCCGCGAGGAGGTG 300
 DB 288 GGCATTCTCTATTAGAAAGCAGTGTGGGCTTCCAGATAAATGCTCCCGCGAGGAGGTG 347
 QY 301 GAGAGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 DB 348 GAGAGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 407
 QY 361 TACGA----- 365
 DB 408 TACGAGAGTGCACGAAGACTTTGCCCATCTTCTGCTGACGAGTGTCTGCTGATGATAA 467
 QY 366 ----- 365
 DB 468 GGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 527
 QY 366 ----- 365
 DB 528 CTGAGTGCCAGCACTGACAGACCCCTGTAGCCAGTGGACCTGTGAGGTACACTATGAG 587
 QY 366 ----- 365
 DB 588 GTCTGCCCCAAGTTTCCCTTAACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 647
 QY 366 --GTTTCAGACACAGTCAAGACTTGTGGCAAGTGTGAGTCCCTTGTGAGATTCACAGCC 423
 DB 648 ACCTTTTTCAGGACCATGTGTAGAGCATGACGAAATGCGGGTCTCTGTGAGATTCACAC 707
 QY 424 ATCGGCTGCTGAGAGCGGTAGAGGTGAGAAACAGCAGGACGACGAGTGTGAGTGTGCTG 483
 DB 708 GTTGGCTGTTTACAGAGATGTTGGAGATGCTGAGAACCTGACGATCATGAGCTGACGGGCTA 767
 QY 484 CGGAGACCTGCGCATGTCTGAGTCTGGTCTGAGGCAAGCCCTCTTGTGGAGAC 543
 DB 768 CGGGAACACCTAGCCCTTACTGCTGAGCTCATCTTGTGAGGCCCAAGCCTCTCCAGGAACC 827

QY 544 CAGAGCCACCGGGGTGAGAGCTCTCTCAGAGGTGCGAGAGCTTGGAGAAAGAACGCGCC 603
 DB 828 TTGAACACAGGTGGGGCCAGAGCTACTCCAGCGGTGCCAGATTTTGGAGCAGAAATAGCA 887
 QY 604 ACTTTTGGAGAACATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
 DB 888 ACTTTTGGAGAACATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 947
 QY 664 GAGCCTGACGCGGCGACGCGCTGAGCAAGACCAAGATTGAGCCCTGAGTAGCAAG 723
 DB 948 GAGCCTGAGCGGCGACGCGCTGAGCAAGACCAAGATTGAGCCCTGAGTAGCAAG 1007
 QY 724 GTGAGCAGCTGAGAGAGAGCATTGGCTCAAGAGACCTGCGGATGGCTGAGTGTGAGCAG 783
 DB 1008 GTGCAACAGCTGAGAGAGAGCATTGGCTCAAGAGACCTGCGGATGGCTGAGTGTGAGCAG 1067
 QY 784 AAGGCTCTTGGAGATGAGGATCCACCTACGATGGGTCTTCTATCTCGAAGATCTCAGAC 843
 DB 1068 AAGGCTCTCGAGTTTGGAGATCCACCTATGATGGGTCTTCTATCTCGAAGATCTCAGAC 1127
 QY 844 TTGCGCAGAGACTCCAGGAAGCTGTGGCTGGCGCATACCGGCATCTTCTCCCGAGCC 903
 DB 1128 TTGCGCAGAGACTCCAGGAAGCTGTGGCTGGCGCATACCGGCATCTTCTCCCGAGCC 1187
 QY 904 TTCTACACCGAGCTACGGCTACAGATGTGTCTGGCTATCTACCTCAACGCGGAGCGC 963
 DB 1188 TTCTACACCGAGCTACGGCTACAGATGTGTCTGGCTATCTACCTCAACGCGGAGCGC 1247
 QY 964 ACCGGGAGAGAAACACCTGCTCTTCTTGTGTGATGAAAGGCGCGGATGAGCGCC 1023
 DB 1248 ACTGGGCGGGAACATCATCTGCTCTTCTTGTGTGATGAAAGGCGCGGATGAGCGCC 1307
 QY 1024 CTGCTGCGGTGGCCCTTCAACGAGAGTGACCTTAATGTGTGCTGCGACCAAGATAACCGG 1083
 DB 1308 CTGTTGAGTGGCCCTTTTATCAGAGATGATGATGATGATGATGATGATGATGATGATG 1367
 QY 1084 GAGCAGTGTATGACGCTTTCAGGCGCGAGCTGATCTTCTTCTTCTTCTTCTTCTTCTTCT 1143
 DB 1368 GAGCATGTGATCGAGCGCATTCAGGCGCGATTCAGGCGCGATTCAGGCGCGATTCAGGCG 1427
 QY 1144 AACGACATGACATCGCAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1203
 DB 1428 AGTGACATGACATCGCAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1487
 QY 1204 AAGAAATTCCTACGTCGCGGAGCGATGCCATCTTCTATCAAGGCGCATTTGAGGAGG 1263
 DB 1488 AAGAAATTCCTACGTCGCGGAGCGATGCCATCTTCTATCAAGGCGCATTTGAGGAGG 1547
 QY 1264 CTCTA 1268
 DB 1548 CTCTA 1552

RESULT 13
 AAT12262
 ID AAT12262 standard; cDNA; 2121 BP.
 XX AC
 XX AAT12262;
 XX DT 09-APR-1996 (first entry)
 XX DE Mouse TRAP2 cDNA.
 XX KW TRAP2; tumour necrosis factor receptor associated factor 2; TNF; CD40;
 XX SS.
 XX OS Mus musculus.
 XX FH Key Location/Qualifiers
 XX FT CDS 48..1553
 XX FT /*tag= a
 XX PN W09533051-A1.

Query Match	55.2%	Score 701	DB 1	Length 2121
Best Local Similarity	71.0%	Pred. No. 2e-164		
Matches 1068	Conservative 0	Mismatches 200	Indels 237	Gaps 1
QY	1	ATGGCTGCAGCTAGCGTGACCGCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTCTCC	60	
DB	48	ATGGCTGCAGCCAGTGTGACTTCCTCTGGCTCCCTAGAACTGCTACAGCTTGGCTTCC	107	
QY	61	AAGACCTCTCTGGGGAACAAGCTGGGAAGCCAAAGTACCTGTGCTCCGCTCGAGAAAGTC	120	
DB	108	AAGACCTCTCTGGGGAACAAGCTGGGAAGCCAAAGTACCTGTGCTCCGCTCGAAAAATC	167	
QY	121	CTCCGAGGCCCTTCCAGGGCGCAGTGTGGCACCGGTACTGCTCTTCTGCTGGCCAGC	180	
DB	168	CTGGGAGGCTTTCAGAGGCCAGTGTGGGACCGCTACTGCTCTTCTGCTGACCGGC	227	
QY	181	ATCCTCAGCTCTGGGCTCTCAAACTGTGCTGCCTGTGTTCAAGAGGCATATATGAAGAA	240	
DB	228	ATCCTCAGCTCTGGGCTCCCAAACTGTGCTGCCTGTGTTCAAGAGGCCTGTATGAAGAA	287	
QY	241	GGCAATTTCTATTTAGAAAGCAGTTCCGCTCTCCAGATAATGCTGCTCCCGCAGGAGGTG	300	
DB	288	GGCAATTTCTATTTAGAGAGTAGTTTCGGCTTTCAGATAACGCTGCCGAGAGAGGTG	347	
QY	301	GAGAGCTCGCGCGCTCTGTCCAGGTGATGATGCACCTGGAGGGGACCTCGAAAGAA	360	
DB	348	GAGAGCTCGCAGCTGTCTGTCCCAATGATGATGCACCTGGAGGGGACCTTGAAGAA	407	
QY	361	TAGCA-----	365	
DB	408	TACGAGAGCTGCCACGAAGGACTTTTGCCCATTCCTGCTGACGGAGTGTCTGCATGTAAA	467	
QY	366	-----	365	
DB	468	GGCTGTGTCGCGCTCAGCGAGAGGAGCACCACTGACGAGGAATGCCCCAAAAGGAGC	527	
QY	366	-----	365	
DB	528	CTGAGCTGCAGCACTCAGAGCACCTGTAGCCACTGTGACCTGGAGGTACACTATGAG	587	
QY	366	-----	365	
DB	588	GTCTGCCCAAGTTTCCCTTAACTGTGTGATGGCTGTGGCAAGAGATCCCTCGGGAG	647	
QY	366	--GTTTCAGAACCAAGTCAAGACTTGTGGCAAGTGTGAGTCCCTTGCAGATTCCAGCC	423	
DB	648	ACGTTTCAGAACCAATGTTAGAGCAATGAGCAAAATGCCGGTTCCTGCAGATTCCACACC	707	
QY	424	ATCGCTGCTCTCAGACCGGTAGAGGGTGAAGAACAGCAGGACGACGAGGTGCAAGTGCGCTG	483	
DB	708	GTTGGCTGTTCAGAGATGGTGGAGACTGAGAACTCTGACAGATCATGAGCTGCAGCGGCTA	767	
QY	484	CGGAGCACTGGCCATGCTACTGAGTCTGGTGTGAGGCAAGGCCCTCTTGGGAGAC	543	
DB	768	CGGAAACACCTTAGCCCTACTGCTGAGCTCAATCTTGGAGGCCCAAGGCTCTCCAGGAACC	827	
QY	544	CAGAGCCACCGGGGTTCAGAGCTCTCCAGAGGTGCGAGAGCTTGGAGAGAGAGACGGCC	603	
DB	828	TTGAAACAGGTGGGCCAGAGCTACTCCAGCGTGTCCAGATTTTGGAGCAGAGATAGCA	887	
QY	604	ACTTTTGAGAACATGTTCTCGTCTTGAAACCGGAGGTGGAGAGGTGGCCATGACTGCC	663	
DB	888	ACCTTTTGAGAACATGTTCTCGTCTTGAAACCGTGAAGTAGAGAGGGTAGCAGTCACTGCA	947	
QY	664	GAGGCTTCAGCGGAGCAGCCGCTCGACCAAGACAAGATTGAAGCCCTGAGTACGCAAG	723	
DB	948	GAGGCTTTAGCCGGCAGCAGCCGCTAGACACAGGACAAGATTGAGGCCCTTGAGTACAG	1007	
QY	724	GTGACAGCTGGAGAGGACATTTGGCCTCAAGSACCTGGCATGGCTGACTTGGAGCAG	783	
DB	1008	GTGCAACAGCTGGAGAGGACATCGGCTCAAGCACTGGCCATGGCTGCTGAGTGGAGCAG	1067	

Qy	784	AAGTCTTGAGAGTGAAGGCATCCACTACGATGGGGTCTTCACTCGGAAGATCTCAGAC	843
Db	1068	AAGGTCTCCGAGTTGGAAGTATCCACCTATGATGGGGTCTTCACTCGGAAGATCTCAGAC	1127
Qy	844	TTGCCACAGGAAGCTCCAGGAAGCTGTGGCTGGCGGCATACCCGGCCATCTTCTCCCCAGCC	903
Db	1128	TTACACAGAAGCGGTACGGAAGCCGTAGCTGGCCGGACACAGGTATCTTCTCCCCAGCC	1187
Qy	904	TTCTACACACAGCAGGTACGGCTACAAGATGTGTCTGCGTATCTACTCTGAACGGCGCAGCC	963
Db	1188	TTCTACACAGCAGATATGGCTACAAGATGTGTCTACGAGTCTACTTTGAATGGCGACGGC	1247
Qy	964	ACGGGCGAGGAACACACACTGTCCCTTCTTTGTTGTTGATGAAGGCGCCGAATGACGCC	1023
Db	1248	ACTGGCGGGAACTCACTGTCTCTCTTTCTGTTGTTGATGAAGGCGCCCAATGATGCT	1307
Qy	1024	CTGTGCGGTGGCCCTTCAACCAAGAGGTGACCTTAAATGCTGCTCGACCAAGAATAACCGG	1083
Db	1308	CTGTTCAGTGGCTTTTAAATCAGAGGTAACATTGATGTTGCTGGACCAATAACAACCGG	1367
Qy	1084	GAGCATGTATTACAGCCTTCAGGCCCGGACGTGACTTCACTCTCTTTTTCAGAGGCCAGTC	1143
Db	1368	GAGCATGTGATGACGCAATTTCAGGCCCGATGTAACCTCGTCTCTTCCAGAGGCCGTGC	1427
Qy	1144	AACGACATGAACATCGCAAGCGGTGCGCCCTCTTTTGCCCGCTCTCCAAAGATGGAGGCA	1203
Db	1428	AGTGACATGACATCGCATGTGCTGCCCTCTTCTGCCCTGTGTCCAAGATGGAGGCC	1487
Qy	1204	AAGAATTCCTACGTGCGGGACGATGCGCATCTTCAATCAAGGCCCATTTGTGGAACCTGACAGG	1263
Db	1488	AAGAATTCCTATGTGCGGGATGATGCGATCTTCAATCAAGCTATTGTGGACCTTAACAGGA	1547
Qy	1264	CTCTA 1268	
Db	1548	CTCTA 1552	

RESULT 5

US-08-744-139-3

; Sequence 3, Application US/08744139

; Patent No. 5869612

; GENERAL INFORMATION:

; APPLICANT: Goedel, David V

; APPLICANT: Roche, Mike

; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/744,139

; FILING DATE: 31-Oct-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/250858

; FILING DATE: 05/27/1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Ginger R.

; REGISTRATION NUMBER: 33,055

; REFERENCE/DOCKET NUMBER: F0897C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-3216

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

RESULT 5

US-08-744-139-3

: Sequence 3. Applic

; Patent No. 5869612

; GENERAL INFORMATION:

; APPLICANT: Goeddel, David v

; APPLICANT: Rothe, Mike

; TITLE OF INVENTION: TUMOR N

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc

STREET: 460 Point San Bruno

CITY: South San Francisco
COUNTY: California

STATE: CALIFORNIA
COUNTRY: USA

COUNTRY: USA
ZTP: 94080

REF: 54000
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch. 1.

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/

SOFTWARE: WinPatIn (Genen)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08

; FILING DATE: 31-Oct-1996

; CLASSIFICATION: 435

;
; PRIOR APPLICATION DATA:

```

;
APPLICATION NUMBER: 08/25
PENDING DATE: 05/07/2004

```

FILING DATE: 05/27/1994
INFORMATION / ACTION INFORMATION

ATTORNEY/AGENT INFORMATION:
NAME: DORCEY CINCOS P

NAME: DLEYER, GILGER K.
REGISTRATION NUMBER: 22 0

REGISTRATION NUMBER: 33,0
REFERENCE/DOCKET NUMBER:

; REFERENCE/DOCID NUMBER:
: TELECOMMUNICATION INFORMATION

TELEPHONE: 415/225-3216

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2121 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-08-744-139-3

Query Match 55.2%; Score 701; DB 2; Length 2121;
 Best Local Similarity 71.0%; Pred. No. 2e-164;
 Matches 1068; Conservative 0; Mismatches 200; Indels 237; Gaps 1;

QY 1 ATGGCTGAGCTAGCGTACCCCTGGCTCCCTGAGTGTCTACAGCCCGCTTCTCC 60
 DB 48 ATGGCTGAGCGAGTGTACTTCCCTGGCTCCCTGAGTGTCTACAGCCCGCTTCTCC 107
 QY 61 AAGACCTCTCGGGGACCAAGCTGGAAGCCCAAGTACCTGTCTCCGCTGCAGAAAGTC 120
 DB 108 AAGACCTCTCGGGGACCAAGCTGGAAGCCCAAGTACCTGTCTCCGCTGCAGAAAGTC 167
 QY 121 CTCGCGAGGCGCTTCCAGCGCAGTGTGGCCACCGGTACTGCTCTTCTGCTGGCCAGC 180
 DB 168 CTGGGAGGCGCTTCCAGCGCAGTGTGGCCACCGGTACTGCTCTTCTGCTGGCCAGC 227
 QY 181 ATCCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTGTGTACAGGCGCATATGAAGAA 240
 DB 228 ATCCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTGTGTATGAAGCGCTGTATGAAGAA 287
 QY 241 GGCATTTCTATTAGAAAGCAGTTCGGCTTCCAGATAATGCTGCCCGCAGGAGGTG 300
 DB 288 GGCATTTCTATTAGAGAGTGTTCGGCTTCCAGATAATGCTGCCCGCAGGAGGTG 347
 QY 301 GAGAGCTTCCCGCGCTGTCTCCAGTATGATGCACTGGAAAGGGAACCTTGAAGAA 360
 DB 348 GAGAGCTTCCCGCGCTGTCTCCAGTATGATGCACTGGAAAGGGAACCTTGAAGAA 407
 QY 361 TAGCA----- 365
 DB 408 TACGAGAGCTGCCAAGAGACTTTGGCCCATTCCTGTGACGAGGTCTCTGATGTAAA 467
 QY 366----- 365
 DB 468 GGCCTGTCCGCTCAGCGAGAGAGGACCACTAGCAGGAAGTCCCAAGAGGAGC 527
 QY 366----- 365
 DB 528 CTGAGCTGCCAGACTGCAGAGCACCCTGTATGACACCTGGACCTGGAGGTACATATGAG 587
 QY 366----- 365
 DB 588 GTCTGCCCCAGTTTCCCTTAACCTGTGTGCTGTGCAAGAGAGATCCCTCGGGAG 647
 QY 366---GTTTCAGGACCACTGCAAGTGTGGCAAGTGTGAGTCCCTTCCAGATTCACGCC 423
 DB 648 ACGTTTCAGGACCACTGTTAGAGCATGCAAGAAATGCCGGTTCCTTCAGATTTCCACCC 707
 QY 424 ATCGCTCCCTCGAGACGGTATGAGGTTGAGAAACAGCAGGAGACGAGGTGCACTGGCTG 483
 DB 708 GTTGGCTGTTTCAAGATGTTGAGACTGAGAACTGCAAGATCATGAGCTGCAGCGCTA 767
 QY 484 CGGAGCACTTGGCCATGCTACTGAGTCTGGTGTGAGGCAAGCCCTTCTTGGGAGAC 543
 DB 768 CGGGAACACCTAGCCCTACTGCTGAGTCTATCTTGGAGGCCCAAGCCTCTCCAGGAAC 827
 QY 544 CAGAGCCACCGGGTCTAGACTCTCAGAGGTGCGAGCCTTGGAGAGAGAGACCGCC 603
 DB 828 TTGAACAGGTGGGCGCAGAGCTACTCAGCGGTGCGAGATTTTGGAGCAGAGATAGCA 887
 QY 604 ACTTTTGAACAATTGTCTGGCTCTGAACCGGAGGTGGAGAGGTGGCCATGACTGCC 663
 DB 888 ACCTTTGAACAATTGTCTGGCTCTGAACCGTGAAGTAGAGAGGTAGCAGTACTGCA 947
 QY 664 GAGGCTGCAGCCGCGCAGCACCCTGGACCAAGCAAGATTGAGCCCTGAGTAGCAAG 723

DB 948 GAGGCTTGTAGCCGCGCAGCACCCTGAGTACAGGACCAAGATTGAGCCCTGAGTAAACAAG 1007
 QY 724 GTGACAGAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGGCGATGGCTGACTTGGAGCAG 783
 DB 1008 GTGCAACAGCTGGAGAGGAGCATCGGCTCAAGGACCTGGCGATGGCTGACTGAGCTGGAGCAG 1067
 QY 784 AAGGCTCTTGGAGATGGAGGAGCATCCACTACGATGGGGTCTTTCATCTGGAAGATCTCAGAC 843
 DB 1068 AAGGCTCTCGAGTTCGAAAGTATCCACCTATGATGGGTCTTCACTCTGGAAGATCTCTGAC 1127
 QY 844 TTGCGCAGAGAGCTCCAGAAAGCTGTGCTGGCGCATACCGCCATCTTCTCCCGCAGCC 903
 DB 1128 TTCAACAGAAAGCTGCAAGAAAGCTGTGCTGGCGCATACCGAGTATCTTCTCCCGCAGCC 1187
 QY 904 TTCTACACAGCAGGTACGGCTTACAAAGATGTCTGCGTATCTACTCTGAAACGGGACGCGC 963
 DB 1188 TTCTACACAGCAGATATGGCTTACAAAGATGTCTACGAGTCTACTTGAATGGCGACGCGC 1247
 QY 964 ACCGCGCAGAGAAACACACTGTCTCTTCTTGTGFGTGAAGAGGCGCCGAAATGACGCC 1023
 DB 1248 ACTGGCGCGGAACTCATCTGTCTCTTCTTGTGFGTGAAGAGGCGCCCAATGATGCT 1307
 QY 1024 CTGCTGCGGTGCGCTTCAACAGAGGTGACCTTAAATGCTGCTGACCAAGAAACCGG 1083
 DB 1308 CTGTTGCAAGTGGCTTTAAATCAGAAAGTAACTGATGTTGCTGGACCATAAACCGG 1367
 QY 1084 GAGCAGCTGATTGAGCCTTTCAGGCGCCGACGTGACTTCACTCTTCTTTCAGAGGCGACTC 1143
 DB 1368 GAGCATGTGATCGAGCATTCAGGCGCGATGAACTGCTCTCTTCCAGAGGCGCTGTC 1427
 QY 1144 AACGACATGAACATCGCAAGCGCTGCGCCCTCTTCTGCGCCGCTCTCCAAGATGGAGCA 1203
 DB 1428 AATGACATGAACATCGCAGTGGCTGCGCCCTCTTCTGCGCCGCTCTCCAAGATGGAGCC 1487
 QY 1204 AAGAAATTCCTAGTGGGAGCAGTCCCATCTTTCATCAAGGCGCATTTGGACCTGACAGGG 1263
 DB 1488 AAGAATTCCTAGTGGGAGTATGCGATCTTCATCAAGCTATTGTCGACCTAACAGGA 1547
 QY 1264 CTCTA 1268
 DB 1548 CTCTA 1552

RESULT 6

US-08-779-599-3

; Sequence 3, Application US/08779599

; Patent No. 6500922

; GENERAL INFORMATION:

; APPLICANT: Goeddel, David V.

; APPLICANT: Rothe, Mike

; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/779,599

; FILING DATE: 07-Jan-1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Ginger R.

; REGISTRATION NUMBER: 33,055

; REFERENCE/DOCKET NUMBER: P0897C2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/325-3216
TELEFAX: 415/952-9681
TELEX: 910/371-7158
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-779-599-3

Query Match 55.2%; Score 701; DB 4; Length 2121;
Best Local Similarity 71.0%; Pred. No. 2e-164;
Matches 1068; Conservative 0; Mismatches 200; Indels 237; Gaps 1;

Qy	1	ATGGCTGCAGCTAGCGTGCACCCCTGGCTCCCTGCAGTGTGCTACAGCCCGGCTTCCTC	60
Db	48	ATGGCTGCAGCCAGTGTGACTTCCCTGGCTCCCTAGAACTGCTACAGCTGCCTTCCTC	107
Qy	61	AAGACCCCTCCTGGGACCAAGCTGGAAGCCAAAGTACCTGTGCTCCGCTGCAGAAACGTC	120
Db	108	AAGACCCCTCCTGGGACCAAGCTGGAAGCCAAAGTACCTGTGCTGCAGCTGCAAAAACATC	167
Qy	121	CTCCGACAGCCCTTCCAGCGCAGTGTGGCCACCGGTACTGCTCTCTGCTGCTGGCCAG	180
Db	168	CTGCGGAGGCCCTTTCAGGCCAGTGTGGCACCCTACTGCTCTCTCTGCTCTGCTGAC	227
Qy	181	ATCCTCAGCTCTGGGCCCTCAGAACTGTGCTGCTCTGTGTTTACGAGGGCATATATGAAGAA	240
Db	228	ATCCTCAGCTCTGGGCCCCAGAACTGTGCTGCTGCTGTCTATGAAAGGCTGTATGAAGAA	287
Qy	241	GGCATTTCTATTTTGAAGCAGTGTGGGCCCTTCCAGATAATGCTGCCCGCAGGGAGTG	300
Db	288	GGCATTTCTATTTTGAAGAGTAGTTTGGGCCCTTCCAGATAACGCTGCCCGCAGAGGTTG	347
Qy	301	GAGAGCTCCCGGCCCTCTGTCCCAAGTATGATGTCACCTGGGAAGGGGACCTCTGAAGAA	360
Db	348	GAGAGCTCCCAAGCTGTCTGTCCCAATGATGATGCACTTTGGAAGGGGACCTTTGAAGAA	407
Qy	361	TACGA-----	365
Db	408	TACGAGAGCTGCCACGAAGGACTTTGGCCCATTTCTGCTGAGGAGTGTCTCGATGTAA	467
Qy	366	-----	365
Db	468	GGCCTGTCCTCGCCTCAGCGAGGAAGGAGCACCACTGAGCAGGAATGCCCAAAAGGAGC	527
Qy	366	-----	365
Db	528	CTGAGCTGCCACACTGACAGACACCTGTAGCCACGTGGACCTGGAGGTACACTATGAG	587
Qy	366	-----	365
Db	588	GTCTGCCCAAGTTTCCCTTAACCTGTGATGGCTGTGGCAAGAAGATCCTTCGGGAG	647
Qy	366	--GTTTTCAGGACCACTCAAGACTTGTGGCAAGTGTGAGTCCCTTGCAGATTCACACGC	423
Db	648	ACGTTTCAGAACCAATTTAGACATGACAAATGCCGGTTTCTCTGCAGATTCACACGC	707
Qy	424	ATCGGTGCTCTGCAGCGGTAGAGGTTGAGAAAACAGCAGGAGCAACGAGTGTGCAGTGGCTG	483
Db	708	GTGGCTGTTCAGATGGTGAGACTCAGAACTTCAGGATCATGAGCTGCAGCGGCTA	767
Qy	484	CGGAGCACCTGGCCATGCTACTGAGCTTCGGTGTGGAGGCAAGCCCTCTTTGGGAGAC	543
Db	768	CGGGAACACTAGCCCTACTCTGAGCTCTTCTTGGAGGCCCAAGCCTCTCCAGGAAC	827
Qy	544	CAGAGCCACCGGGGTACAGCTCTGAGAGGTCGAGAGCTGAGAGAGAGACCGGCC	603
Db	828	TTGAACACAGGTGGGGCCAGACTACTCAGCGGTTGCCAGATTTTGGAGCAGAGATAGCA	887
Qy	604	ACTTTTGAACAATTTGCTGCTGCTGAACCGGAGGTGGAGAGGGTGGCCATGACTGCC	663

```

RESULT 7
PCT-US95-06639-3
; Sequence 3, Application PC/TUS9506639
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06639
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858

```

```

; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION NUMBER: 08/331394
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2121 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-06639-3

Query Match          55.2%; Score 701; DB 5; Length 2121;
Best Local Similarity 71.0%; Pred. No. 2e-164;
Matches 1068; Conservative 0; Mismatches 200; Indels 237; Gaps 1;

QY 1 ATGGCTGAGCTAGGTGACCCCGCTGGCTCCCTGAGTGTCTACAGCCGGCTTCTCC 60
DB 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 48 ATGGCTGAGCCAGTGTGACTTCCCGCTGGCTCCCTAGAACTGTCTACAGCCCTTCTCC 107
DB 48 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AAGACCTCTCTGGGAGCCAGCTGGAAGCCAGTACCTGTCTCCGCTCCAGAAAGTTC 120
DB 61 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 108 AAGACCTCTCTGGGAGCCAGCTGGAAGCCAGTACCTGTCTCCGCTCCAGAAAGTTC 167
DB 108 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CTCGCGAGCCCTTCCAGCGCCAGTGTGGCCACCGCTACTGCTCTCTCTGCTGGCCAGC 180
DB 121 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 168 CTGGCGAGGCGCTTCCAGCGCCAGTGTGGCCACCGCTACTGCTCTCTCTGCTGGCCAGC 227
DB 168 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 228 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 287
DB 228 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 GGCATTTCTATTAGAAAGCAGTTCGGCTCTCCAGATATGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 288 GGCATTTCTATTAGAGAGTAGTTCGGCTCTCCAGATATGCTGCTGCTGCTGCTGCTGCTGCTG 347
DB 288 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 GAGAGCTGCGCGGCTGTGCTCAGTGTGATGCACTGGAAGGGGACCTTGAAGAA 360
DB 301 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 348 GAGAGCTGCGCGGCTGTGCTCAGTGTGATGCACTTGAAGGGGACCTTGAAGAA 407
DB 348 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 TACGA----- 365
DB 361 |||||
QY 408 TACGAGAGCTGCCAGAGAGACTTTGGCCATTCCTGCTGAGGAGTGTCTGCTGATGA 467
DB 408 |||||
QY 366 ----- 365
DB 366 -----
QY 468 GGCCTGTGCTGCTCAGCGAGAGAGGACCACTGAGCAGGAAATGCCCCAAAGGAGC 527
DB 468 |||||
QY 366 ----- 365
DB 366 -----
QY 528 CTGAGCTGCCAGCACTGCGAGAGCACTGTAGCCACCTGAGCCTGGAGGTACACTATGAG 587
DB 528 |||||
QY 366 ----- 365
DB 366 -----
QY 588 GTCTGCCCAAGTTTCCCTTAACCTGTGATGGCTGTGCGAAGAAAGATCCCTCGGGAG 647
DB 588 |||||
QY 366 --GTTTCAGGACCACTGAGACTGTGGCAAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 423
DB 366 |||||
QY 648 ACCTTTTTCAGGACCACTGTAGAGCACTGAGCAAAATGCCGGTTCCTGCTGCTGCTGCTGCTGCTG 707
DB 648 |||||
QY 424 ATCCGCTGCTCGAGAGCGGTAGAGGTTGAGAAACAGCAGCAGGACCAAGGAGTGTGCTGCTGCTGCTG 483
DB 424 |||||
QY 708 GTTGGCTGTTTCAGAGATGTTGAGACTGAGAACTGAGCACTGAGCACTGAGCACTGAGCACTGAGCACTG 767
DB 708 |||||
QY 484 CGGAGGACCTTGGCCCTGCTACTGAGCTCGGTGTGGAGCAAGCCCTCTTTGGGAGAC 543
DB 484 |||||

```

RESULT 8

US-09-167-109-1

; Sequence 1, Application US/09167109

; Patent No. 6399297

; GENERAL INFORMATION:

; APPLICANT: Baker, Brenda F.

; APPLICANT: Cowser, Lex M.

; APPLICANT: Monia, Brett P.

; APPLICANT: Xu, Xiaoxing S.

; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION

; FILE REFERENCE: ISPH-0321

; CURRENT APPLICATION NUMBER: US/09/167,109

; NUMBER OF SEQ ID NOS: 228

; SEQ ID NO 1

; LENGTH: 2380

; TYPE: DNA

```
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (76)..(1326)
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: U19261 Genbank
/ DATABASE ENTRY DATE: 1995-02-21
/ US-09-167-109-1

Query Match      23.4%; Score 296.6; DB 3; Length 2380;
Best Local Similarity 66.2%; Pred. No. 4.5e-64;
Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

QY 586 CTGGAGAGAGAGCGCCACTTTTGAGAACATTTCTGCGTCTCAACCGGAGGTGGAG 645
Db      |||||
QY 643 CTGGAGGGAGAGCTGCGTGTGTTTGAGAACATTTGCTCTCAACAGGAGGTGGAG 702
Db      |||||
QY 646 AGGGTGGCCATGATGCGCGAGGCTGCAGCGCGGAGCAGCGCTGGACCAAGACAAATT 705
Db      |||||
QY 703 GCCTCCACCTGGCGCTGGCCACCTCTATCCACAGAGCCAGCTGGACCGCATC 762
Db      |||||
QY 706 GAAGCCTGAGTAGCAAGGTGCAGCAGCTGAGAGGAGCATTTGGCCTCAAGGACTGGCG 765
Db      |||||
QY 763 CTGAGCTTGGAGCAGAGGTTGGAGCTTCAGCAGACCTTGGCCCAAGAAAGACAGGCC 822
Db      |||||
QY 766 ATGGCTGACTTTGGAGCAGAGGCTTTGGAGATGGAGGATCCACCTACGATGGGTCTTC 825
Db      |||||
QY 823 CTGGCAAGCTGGAGCAGAGCTTGGAGCTTCAGCAGACCTTGGCCCAAGAAAGACAGGCC 882
Db      |||||
QY 826 ATCTGGAGATCTCAGACTTCGCCAGGAGCTCCAGGAAGCTGGTGGCTGGCCGATACCC 885
Db      |||||
QY 883 CTGTGGAAGATCACAATGTACCAGGGGTGCCATGATGCGCTTCCGCTGACCTAAGCTCAGCG 942
Db      |||||
QY 886 GCCATCTTCTCCAGCGCTTCTACACCCAGCAGGTACGGCTACAGATGTGTCTCGGTATC 945
Db      |||||
QY 943 AGCCTCTTCTCCAGCGCTTCTACATGCCAAGTATGGCTACAAAGTGTGTGCGGTG 1002
Db      |||||
QY 946 TACTTGAACGGCGAGCGGACCGGGGAGGAGAACACACTGTCTCTCTTTTGTGGTGTG 1005
Db      |||||
QY 1003 TACTTGAATGGAGATGGCACTGGAAAGAGAACCCATCTGTCTCTTTCATCGTATCATG 1062
Db      |||||
QY 1006 AAGGCGCCGAATGAGCGCTCTGCTGGTGGGCCCTTCAACAGAAAGGTGACCTTAATGTG 1065
Db      |||||
QY 1063 AGAGGGAGATGATGATGCGCTGCTGCGGTGGCCCTTCCGGAACAGGTACACCTTTCATG 1122
Db      |||||
QY 1066 CTCGACCAAGATAACCGGGAGCAGCTGATTAGCGCTTTCAGGCGCCGAGCTGACTTCATCC 1125
Db      |||||
QY 1123 CTGGACCAAGAACACCGGTGAGCAGCGCATTTGACGCTTCCGCGCTTCCGCGCTGACG 1182
Db      |||||
QY 1126 TCTTTTTCAGAGGCGAGTCAACGACATGAACATCGCAAGCGGCTGCCCTCTTCTGCCCC 1185
Db      |||||
QY 1183 TCCTTCAGAGGCGCCAGAGTGAAACCAACGTCGCGAGTGATGCCACTCTTCTTCCCC 1242
Db      |||||
QY 1186 GTCTCCAGATGGAGGCA---AAGAAATTCCTAGCTGGGAGCATGCCATCTTCATCAAG 1242
Db      |||||
QY 1243 CTGAGCAAACTGCAGTCAACCAAGACGCGCTACGTGAAGAGACACAAATGTTCTCAAG 1302
Db      |||||
QY 1243 GCCATTGTGGA 1253
Db      |||||
QY 1303 TGCAATTGTGA 1313
Db      |||||
```

RESULT 9

```
PCT-US95-16980-2
Sequence 2, Application PC/TUS9516980
GENERAL INFORMATION:
APPLICANT: Brigham & Women's Hospital
TITLE OF INVENTION: CONTROLLING TRAP-MEDIATED SIGNALS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
```

```
/ STATE: MA
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30B
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/16980
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/367,540
/ FILING DATE: 30-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Freeman, John W.
/ REGISTRATION NUMBER: 29,066
/ REFERENCE/DOCKET NUMBER: 05311/014W01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)542-5070
/ TELEFAX: (617)542-8906
/ TELEX: 100254
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2380 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 76..1323
/ PCT-US95-16980-2
```

Query Match 23.4%; Score 296.6; DB 5; Length 2380;

Best Local Similarity 66.2%; Pred. No. 4.5e-64;

Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

```
QY 586 CTGAGAGAGAGAGCGCCACTTTTGAGAACATTTCTGCGTCTCTGAGACCGGAGGTGGAG 645
Db      |||||
QY 643 CTGAGGGAGAGCTGCGTGTGTTTGAGAACATTTGCTCTCAACAGGAGGTGGAG 702
Db      |||||
QY 646 AGGGTGGCCATGATGCGCGAGGCTGCAGCGCGGAGCAGCGCTGGACCAAGACAAATT 705
Db      |||||
QY 703 GCCTCCACCTGGCGCTGGCCACCTCTATCCACAGAGCCAGCTGGACCGCATC 762
Db      |||||
QY 706 GAAGCCTGAGTAGCAAGGTGCAGCAGCTGAGAGGAGCATTTGGCCTCAAGGACTGGCG 765
Db      |||||
QY 763 CTGAGCTTGGAGCAGAGGTTGGAGCTTCAGCAGACCTTGGCCCAAGAAAGACAGGCC 822
Db      |||||
QY 766 ATGGCTGACTTTGGAGCAGAGGCTTTGGAGATGGAGGATCCACCTACGATGGGTCTTC 825
Db      |||||
QY 823 CTGGCAAGCTGGAGCAGAGCTTGGAGCTTCAGCAGACCTTGGCCCAAGAAAGACAGGCC 882
Db      |||||
QY 826 ATCTGGAGATCTCAGACTTCGCCAGGAGCTCCAGGAAGCTGGTGGCTGGCCGATACCC 885
Db      |||||
QY 883 CTGTGGAAGATCACAATGTACCAGGGGTGCCATGATGCGCTTCCGCTGACCTAAGCTCAGCG 942
Db      |||||
QY 886 GCCATCTTCTCCAGCGCTTCTACACCCAGCAGGTACGGCTACAGATGTGTCTCGGTATC 945
Db      |||||
QY 943 AGCCTCTTCTCCAGCGCTTCTACATGCCAAGTATGGCTACAAAGTGTGTGCGGTG 1002
Db      |||||
QY 946 TACTTGAACGGCGAGCGGACCGGGGAGGAGAACACACTGTCTCTCTTTTGTGGTGTG 1005
Db      |||||
QY 1003 TACTTGAATGGAGATGGCACTGGAAAGAGAACCCATCTGTCTCTTTCATCGTATCATG 1062
Db      |||||
QY 1006 AAGGCGCCGAATGAGCGCTCTGCTGGTGGGCCCTTCAACAGAAAGGTGACCTTAATGTG 1065
Db      |||||
QY 1063 AGAGGGAGATGATGATGCGCTGCTGCGGTGGCCCTTCCGGAACAGGTACACCTTTCATG 1122
Db      |||||
QY 1066 CTCGACCAAGATAACCGGGAGCAGCTGATTAGCGCTTTCAGGCGCCGAGCTGACTTCATCC 1125
Db      |||||
QY 1123 CTGGACCAAGAACACCGGTGAGCAGCGCATTTGACGCTTCCGCGCTTCCGCGCTGACG 1182
Db      |||||
QY 1126 TCTTTTTCAGAGGCGAGTCAACGACATGAACATCGCAAGCGGCTGCCCTCTTCTGCCCC 1185
Db      |||||
QY 1183 TCCTTCAGAGGCGCCAGAGTGAAACCAACGTCGCGAGTGATGCCACTCTTCTTCCCC 1242
Db      |||||
QY 1186 GTCTCCAGATGGAGGCA---AAGAAATTCCTAGCTGGGAGCATGCCATCTTCATCAAG 1242
Db      |||||
QY 1243 CTGAGCAAACTGCAGTCAACCAAGACGCGCTACGTGAAGAGACACAAATGTTCTCAAG 1302
Db      |||||
QY 1243 GCCATTGTGGA 1253
Db      |||||
QY 1303 TGCAATTGTGA 1313
Db      |||||
```

QY 1126 TCTTTTCAGAGGCCAGTCAACGACATGAACATCGCAAGCGGTGCCCCCTCTTCTGCCCC 1185
 DB 1183 TCTTTTCAGAGGCCAGTCAACGACATGAACATCGCAAGCGGTGCCCCCTCTTCTGCCCC 1242
 QY 1186 GTCTCCAGATGGAGGCA---AAGAAATTCCTACGTGCGGAGCATGCAATCTTCATCAAG 1242
 DB 1243 CTCAGCAAACTGCAGTCAACCAAGCAAGCGCTACGTGAAGGACGACACAATGTTCTCTCAAG 1302
 QY 1243 GCCATTGTGGA 1253
 DB 1303 TCCATTGTGGA 1313

RESULT 10

US-08-705-771-7
 ; Sequence 7, Application US/08705771
 ; Patent No. 6054289
 ; GENERAL INFORMATION:

APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
 APPLICANT: Jian Ni and Jing-Shan Hu
 TITLE OF INVENTION: Human Genes, Sequences and
 TITLE OF INVENTION: Expression Products
 NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/705,771

FILING DATE: August 30, 1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-346 (PFI96)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 973-994-1700

TELEFAX: 973-994-1744

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 2361 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-705-771-7

Query Match 21.8%; Score 276.8; DB 3; Length 2361;
 Best Local Similarity 64.3%; Pred. No. 3.7e-59;
 Matches 431; Conservative 0; Mismatches 237; Indels 2; Gaps 1;

QY 586 CTGAGAGAGAGAGCGGCACCTTTGAGAAATGCTGCGCTCTGAAACCGGAGGTGGAG 645
 DB 645 CTGAGGGGAGGTGCGGTGTTGAGAAATGTTGCTCTCTCAACAGGAGGTGGAG 704
 QY 646 AGGTGCGCCATGACTGCGGAGGCGCTGAGCGGCGAGCACCGGCTGACCAAGACAGATT 705
 DB 705 GCCTCCACCTGGCCCTGCGCCACTCTATCCACGAGGACAGTGGACCGTGAAGCCATC 764
 QY 706 GAAGCCCTGAGTAGCAGGTGACAGCTGGAGGAGGACATTTGGCTCTAAGGACCTGGCG 765
 DB 765 CTGAGCTTGGAGCAGAGGGGTGGTGCAGGTTTCAGCAGACCCCTGCGCCAGAAAGACGAGGC 824

QY 766 ATGGCTGACTTGGAGCAGAGAGGTCTTGAGATGGAGGCATCCACTAGATGGGGTCTTC 825
 DB 825 CTGGGCAAGCTGGAGCAGAGCTTGGCGCTCATGGAGAGGCGCTCTTCGATGGCACTTTC 884
 QY 826 ATCTGGAAGATCTCAGACTTCCGAGAGAGCTCCAGGAAGCTGTGGCTGGCGGCATACCC 885
 DB 885 CTGTGGAAGATCACCAGTGTCCACGAGGCGGTGCCATGATCGGCTGTGGCAGGACCGTC 944
 QY 886 GCATCTTCTCTCCCGAGCCTTTACACACGACAGGTACGGCTACAGATGTGTCTGGGTATC 945
 DB 945 AGCTCTTCTCTCCCGAGCCTTTACACTGCCAAGTATGCTACAGTTGTGTGGCTGGGTG 1004
 QY 946 TACCTGAACGGGACGGACACCGGGGAGAGAACACACTGTGTCCCTCTTCTTTGTGGTGATG 1005
 DB 1005 TACCTGATTGGAGATGGCACCTGGAAGAGAACCCATCTTTGCTCTTCATCGTATCATG 1064
 QY 1006 AAGGGCCGAATGACGCGCTGTGCGGTGGCGCTTCAACAGAGGTGACCTTAAATGCTG 1065
 DB 1065 AGAGGGAGTATGATGCGCTGCTGCGGTGGCGCTTCCGGAACAAGTCACTTCATGCTG 1124
 QY 1066 CTCGACCAAGATTAACGGGAGCACGTGATTGACGCTTTCAGGCCGAGCTGACTTCATCC 1125
 DB 1125 CTGGACCAAGAACACCGTGAGCAGCCCATTTAGCGCTTCCGGCCCTGACCTAAGCTCAGCG 1184
 QY 1126 TCTTTTCAGAGGCCAGTCAACGACATGAACATCGCAAGCGGTGCGCCCTCTTCTGCCCC 1185
 DB 1185 TCTTCCAGAGGCCCCAGAGTGAACCAACGTGGCAGTGGATGCCCACTCTTCTTCCCC 1244
 QY 1186 GTCTCCAGATGGAGGCAAGAAATTCCTAC--GTGCGGAGGATGCCCATCTTTCATCAAGG 1243
 DB 1245 CTCAGCAAACTGCAGTCACCCCAAGCACGCTAGTGAAGGACGACACAATGTTCTCAAGT 1304
 QY 1244 CCATTGTGGA 1253
 DB 1305 GCATTGTGGA 1314

RESULT 11

US-09-417-540-7

; Sequence 7, Application US/09417540

; Patent No. 6639052

; GENERAL INFORMATION:

APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,

Jian Ni and Jing-Shan Hu

TITLE OF INVENTION: Human Genes, Sequences and

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/417,540

FILING DATE: 14-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,771

FILING DATE: August 30, 1996

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-346 (PFI96)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 973-994-1700

TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 7;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-417-540-7

Query Match 21.8%; Score 276.8; DB 4; Length 2361;
Best Local Similarity 64.3%; Pred. No. 3.7e-59;
Matches 431; Conservative 0; Mismatches 237; Indels 2; Gaps 1;

QY 586 CTGGAGAAAGACGCGCACTTTGAGACATGTCGCTCCTGAACCGGAGGTGGAG 645
DB 645 CTGGAGGGAAGCTGCGTGTGTTGAGAACATGTTGCTGCTCAACAGGAGGTGGAG 704
QY 646 AGGGTGGCCATGACTGCCGAGGCGCTGCAGCGGCGAGCACCGGCTGGACCAAGCAAGATT 705
DB 705 GCCTCCCACTGGCCCTGGCCACTCTATCCACAGAGCCAGCTGACCGTGAGCGCATC 764
QY 706 GAAGCCCTGAGTAGAAGGTGAGCGAGCTGGAGAGAGCATTTGGCTCAGGACCTGGCG 765
DB 765 CTGAGCTTGGAGCAGAGGCTGTGTCAGGTTTCAGCAGACCCCTGCCAGAAAGACGAGCC 824
QY 766 ATGCTGACTTGGAGCAGAGGCTTTGGAGATGGAGGCATCCACCTACGATGGGTCTTTC 825
DB 825 CTGGGCAAGCTGAGCAGAGCTTGGCCCTCATGGAGAGGCTCTCTTCATGGCACTTTC 884
QY 826 ATCTGGAAGATCTCAGACTTGGCCAGAGAGCTTCAGGAAGCTGTGGCTGGCGCATACCC 885
DB 885 CTGTGGAAGATCAACAGTGTCAACAGGCGGTGCGCATGAGTCGGCCCTGTGGCAGGACCGTC 944
QY 886 GCATCTTCTCCCGCCTTCTACACAGCAGTACGCTACAGATGTTGTTGCGTATC 945
DB 945 AGCCTCTTCTCCCGCCTTCTACCTGCCAGTATGCTGCAAGTTGCTGCGGCTG 1004
QY 946 TACCTGAAACGGCGACCGGCGGCGAGGAACACACCTGTCCCTCTTCTTGTGFGATG 1005
DB 1005 TACCTGATTGGAGATGGCATGGAAGAGAACCATCTTTGCTCTTCATCGTATCATG 1064
QY 1006 AAGGGCCGAGTACGCGCTGCTGCGGTGGCCCTTCAACAGAGGTGACCTTAATGCTG 1065
DB 1065 AGAGGGGAGTATGATGCTGCTGCGGTGGCCCTTCCGGAACAGGTACCTTTCATGCTG 1124
QY 1066 CTGACCAAGATTAACCGGAGCAGCTGATTGACGCTTTCAGGCGCCGACGTGATTCATCC 1125
DB 1125 CTGGACCAAGAACACCTGTGAGCAGCCATTTGACGCTTCGGGCTGACCTAAGCTCAGCG 1184
QY 1126 TCTTTTCAGAGGCGAGTCACAGCAGATGAACATCGAAGGGCTGCGCCCTCTTCTGCCCC 1185
DB 1185 TCCTTCCAGAGGCGGCGAGAGTGAACCAACAGTGGCCAGTGGATGCGCACTCTTCTTCCCC 1244
QY 1186 GTCTCCAGATGGAGGCAAGATTCCTAC -GTGGGAGCAGTGCATCTTCATCAAGG 1243
DB 1245 CTAGCAAACTGAGTACCCAGACGCGCTACGTAAGGACGACAAATGTTCTCTAGT 1304
QY 1244 CCATTGTGGA 1253
DB 1305 GCATTGTGGA 1314

RESULT 12
US-08-331-394-1
; Sequence 1, Application US/08331394
; Patent No. 5670319
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-Associated Factors

NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,394
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250858
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-331-394-1

Query Match 21.4%; Score 272; DB 1; Length 2088;
Best Local Similarity 63.8%; Pred. No. 5.5e-58;
Matches 429; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 586 CTGAGAAAGAGAGCGGCCACTTTTGAAGAACATTTCTCGCTCTGAAACCGGAGGTGGAG 645
DB 773 CTGGAGGAGAGAGCTGCGTGTGTTTGAACACATTTGCTGCTCTCAACAGGAAAGTGGAG 832
QY 646 AGGGTGGCCATGACTGCCGAGGCGCTGCAGCGGCGAGCACCGGCTGGACCAAGCAAGATT 705
DB 833 GCTTCCCACTTGGCACTGGCCGCTTCCATCCACAGAGCCAGTTGGACCGAGACACCTC 892
QY 706 GAAGCCCTGAGTAGCAAGGTGCAGCGCTGGAGAGGAGCATTTGGCCTCAAGGACCTGGCG 765
DB 893 CTGAGCTTGGAGCAGAGGCTGTGGAATTAACAGCAAAACCTTGGCTCAAAAAGACAGGTC 952
QY 766 ATGCTGACTTGGAGCAGAAAGTCTTGGAGATGGAGGCATCCACCTAGATGGGCTCTTC 825
DB 953 CTGGCAAGCTTGAGCAGCTGCGCATGAGGAGGAGGATCCTTTGATGGTACTTTC 1012
QY 826 ATCTGGAAGATCTCAGACTTCCGAGGAAGTCCAGGAAGCTGTGGCTGGCGCATACCC 885
DB 1013 CTGTGGAAGATCAACCAATGTACCAAGCGGTGCCACGAGTCAAGTGTGTGGCCGACTGC 1072
QY 886 GCCATCTTCTCCCGCCTTCTACACAGAGGTACGCTACAGATGTGTCTCGGTATC 945
DB 1073 AGCCTCTTCTCTCCAGCTTTCTACACTGCCAAGTATGGTTTCAAGTTGTGGCTGGCTTG 1132
QY 946 TACCTGAAACGGGCGGCGACCGGCGGAGGAACACACCTGTCCCTCTCTTTTGTGGTATG 1005
DB 1133 TACCTGAAACGGGATGGCTCAGGCAAGAGAGACCCACCTGTCCCTCTTCATCGTATCATG 1192
QY 1006 AAGGGCCGGAATGACGCGCTGTCTGGGTGGCCCTTCAACAGAGGTGACCTTAATGCTG 1065
DB 1193 AGAGGAGAAATACGATGCTCTCTGCGCTGGCCCTTTCAGGAAACAGGTCACTTTATGCTA 1252
QY 1066 CTCGACCAAGATAACCGGGAGGACGACGTGATTGACGCTTCAGGCCCGACGCTGACTTCATCC 1125

Db 1253 CTGACCAAGAACCGAGAGCATGCTATGTAGCTTCCTCGGCTGACCTGAGCTCAGCC 1312
 QY 1126 TCTTTTCAGAGCCAGTCAACACATGCAATCGCAAGCGGCTGCCCTCTTCTGCCCC 1185
 Db 1313 TCTTCCAGCGCCACAGAGTGAACCAAGTGGCGGCTGCCCTCTTCTTCCCC 1372
 QY 1186 GTCTCCAGATGAGGCA---AAGAAATTCCTACGTGCGGAGCATGCTCATCAAG 1242
 Db 1373 CTCAGAGCTGCAATCAACCAAGCAAGCTACGTCACCAAGATGACACAATGTTCTCAAA 1432
 QY 1243 GCCATTGTGGAC 1254
 Db 1433 TGCATTGTGGAC 1444

RESULT 13

US-08-250-858-1
 ; Sequence 1, Application US/08250858
 ; Patent No. 5708142
 ; GENERAL INFORMATION:
 ; APPLICANT: Goedel, David V.
 ; APPLICANT: Rothe, Mike
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
 ; NUMBER OF SEQUENCES: 62
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/250.858
 ; FILING DATE: 27-May-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: 897.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-3216
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2088 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-250-858-1

Query Match 21.4%; Score 272; DB 1; Length 2088;
 Best Local Similarity 63.8%; Pred. No. 5.5e-58;

Matches 429; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 586 CTGAGAGAGAGCGGCCACTTTGAGAACATTTCTGCGTCTGAACCGGAGGTGGAG 645
 Db 773 CTGAGAGAGAGCTGCGTGTGTTGCAACATTTGCTCTCAACAGAGAGTGGAG 832
 QY 646 AGGTGCGCATGCTGCGGAGCTGCGCGGAGCAGCTGCAACCAACAGATT 705
 Db 833 GCTTCCACCTGGCACTGGCGGCTCTCATCCACGAGCGAGTTGACCGAGCACCTC 892
 QY 706 GAAGCCCTGAGTAGCAAGTGTGAGAGTGGAGGAGGAGCATTTGGCTCAAGGACCTGGCG 765

Db 893 CTGAGCTTGGAGCAGAGGTGGTGAATTTACAGCAAAACCTGGCTCAAAAAGACAGGTC 952
 QY 766 ATGCTGACTTGGAGCAGAGGTCTTGGAGATGGAGGATCCACCTACGATGGGTCTTC 825
 Db 953 CTGGGCAAGCTTGGACACAGTCTGCGACTCATGGAGGAGGCATCCTTTGATGGTACTTTC 1012
 QY 826 ATCTGAAGATCTCAGACTTCGCGAGGAAGCTCCAGGAAGCTGTGGCTGGCGCATACCC 885
 Db 1013 CTGTGAAGATCACCAATGTCCAGCGGTGCCAGAGTCAAGTGTGGCGGAGTGTTC 1072
 QY 886 GCATCTTCTCCAGCCTTCTACACGACAGGTACGGCTACAAGATGTTCTGGTATTC 945
 Db 1073 AGCCTCTTCTCCAGCTTCTACACTGCCAAATATGTTTACAAGTGTGGCTGGCTTG 1132
 QY 946 TACCTGAACGGGACGGCACCGGCGGAGGAACACACCTGTGCTCTTCTTGTGGTGTG 1005
 Db 1133 TACCTGAACGGGATGGCTCAGGCAAGAGACCCACTGTCTCTTCTCATGTGATCATG 1192
 QY 1006 AAGGCCCCGAATGACGCCCTGTGCGGTGGCCCTTCAACAGGAAGTGAACCTTAATCTG 1065
 Db 1193 AGAGGAGATACGATGCTCTCTGCTGCTGGCTTTCAGGAACAAGTCACTTTATGCTA 1252
 QY 1066 CTCGACCAAGTAACCGGAGCAGCTGATTGACGCTTTCAGGCGGAGTGTGACTTCATCC 1125
 Db 1253 CTGACCAAGAACACCGAGAGCATGCTATTGATGCTTCCGCGCTGAGCTGAGCTCAGCC 1312
 QY 1126 TCTTTTCAGAGCCAGTCAACGACATGAACATGCAAGCGGTGCGCCCTCTTCTTGCCTCC 1185
 Db 1313 TCTTCCAGCGCCACAGAGTGAGACCAAGTGGCCAGCGCTGCTCTTCTTCTCC 1372
 QY 1186 GTCTCCAGATGGAGGCA---AAGAAATTCCTACGTGCGGAGCATGCCATCTTCAATCAAG 1242
 Db 1373 CTCAGAACTGTCAGTCAACCAAGCAAGCTACGCTACCAAGATGACACAATGTTCTCAAA 1432
 QY 1243 GCCATTGTGGAC 1254
 Db 1433 TGCATTGTGGAC 1444

RESULT 14

US-08-446-915-1
 ; Sequence 1, Application US/08446915
 ; Patent No. 5741667
 ; GENERAL INFORMATION:
 ; APPLICANT: Goedel, David V.
 ; APPLICANT: Rothe, Mike
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446.915
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/250858
 ; FILING DATE: 27-May-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/331394
 ; FILING DATE: 28-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.

/	REGISTRATION NUMBER:	33,055
/	REFERENCE/DOCKET NUMBER:	897P2
/	TELECOMMUNICATION INFORMATION:	
/	TELEPHONE:	415/225-3216
/	TELEFAX:	415/952-9881
/	TELEX:	910/371-7168
/	INFORMATION FOR SEQ ID NO: 1:	
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH:	2088 bases
/	TYPE:	nucleic acid
/	STRANDEDNESS:	single
/	TOPOLOGY:	linear
/	US-08-446-915-1	
Query Match		
Best Local Similarity 63.8%; Pred. No. 5.5e-5;		
Matches 429; Conservative 0; Mismatches 240; Indels 3; Gaps 1;		
QY	586	CTGGAGAGAAGACGGCCACTTTTGAAACAATTGTCGTGCCTCTGTGAACCGGAGGTGGAG 645
DB	773	CTGGAGAGAAGTGCCTGTGTTTGGCAACAATGTTGCTGTCTCACAAGGAAGTGGAG 832
QY	646	AGGTGTGCCATGACTGCGGAGGCTGCAGCGGCAGCACCGGCTGGACCAGACAAGATT 705
DB	833	GCTTCCCACCTGGCACTGGCGGCTCATCCAACAGAGCCAGTTGGACCGAGCCACTC 892
QY	706	GAAGCCCTGAGTAGCAAGGTGCACAGCTGGAGAGGAGCATTTGCCCTCAAGGACCTGGCG 765
DB	893	CTGAGCTTGGAGCAGAGGGTGGTAATTACAGCAAACCTTGGCTCAAAAAGACCAGGTC 952
QY	766	ATGGCTGACTTGGAGCAGAGGCTTTGGAGATGGAGCATCCACCTACGATGGGTCTTC 825
DB	953	CTGGGCAAGCTTGAGCAAGTCTCGCACTCATGGAGGAGGATCCCTTTGATGTACTTTC 1012
QY	826	ATCTGGAAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGTGGCTGGCCCGCATACC 885
DB	1013	CTGTGGAAGATCACCATTGTCACCAAGCGGTGCCACGAGTCAGTGTGTGCCCGACTGTC 1072
QY	886	GCCATCTTCCCGAGCTTCTAACACAGAGGTACGGCTTACAAGATGTGTCTGCGTATC 945
DB	1073	AGCCTCTCTCTCCAGCTTTCTACACTGCCAAGTATGGTTACAAAGTTGTGCCTGCGCTG 1132
QY	946	TACCTGAACGGCAGCGCACCGGCGAGGAACACACCTGTCCCTCTCTTTTGTGGTCA TG 1005
DB	1133	TACCTGAACGGGGATGGCTCAGGCAAGAACCCACTGTCCCTCTCTCATGTGATCATG 1192
QY	1006	AAGGGCCGAATGACGCCCTGCTCGGTGGSCCTTCAACACAGAGGTGACCTTAATGCTG 1065
DB	1193	AGAGGAAATACGATGCTCTCTCTGCCCTTTCAGGAACAAGTCACCTTATGCTA 1252
QY	1066	CTCGACAGAAATAACGGGAGCAGCTGATTTGACGCTTTCAGGCCCGAGGTGACTTCATCC 1125
DB	1253	CTTGACCAGAACAAACCGAGACATGCTATTGATGCCTTCGGGCTGCACCTGAGCTCAGCC 1312
QY	1126	TCCTTTTCAGAGCCAGTCAACGACATGAACATCCCAAGCGGCTGCCCTCTCTTCGCCCC 1185
DB	1313	TCCTTTCAGCGGGCACAGAGTGAGACCAACTGGCCAGCGGCTGCCGCTCTCTTCTCCCC 1372
QY	1186	GTCTCCAGATGGAGGCA---AAGAAATTCCTACGTGGGGGACGATGCCATCTTCATCAAG 1242
DB	1373	CTCAGCAAGCTGCAGTCAACCAAGCAGCGCTACGTCAAGAGATGACACAATGTTCTCTCAA 1432
QY	1243	GCCATTGPGGAC 1254
DB	1433	TGCATTGPGGAC 1444

RESULT 15
US-08-744-139-1
; Sequence 1, Application US/08744139
; Patent No. 5869612
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V

APPLICANT: Roche, Mike
 TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/744,139
 FILING DATE: 31-Oct-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/250858
 FILING DATE: 05/27/1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Drzger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P0897C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-3216
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2088 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-08-744-139-1

Query Match	21.4%	Score 272	DB 2	Length 2088	
Best Local Similarity	63.8%	Pred. No. 5.5e-58			
Matches 429	Conservative	0	Mismatches 240	Indels 3	Gaps 1
QY	586	CTGAGAGAAGACGGCCACTTTTGAAACATTTGTCTGGCTCTCGAACCGGAGGTGGAG	645		
DB	773	CTGGAGGAGAAGCTGGGTGTTTGCACATTTGTCGTCTCTCAACAGGAAGTGGAG	832		
QY	646	AGGTGGCCATGACTGCCGAGGCTGTGAGCGCGGACGACCGGCTGGAACCAAGACAGATT	705		
DB	833	GCATTCCACCTGGCACTGGCGGCTCCATCCAGCAGAGCCAGTTGGACCGAGAGCACCTC	892		
QY	706	GAAGCCCTGAGTAGCAAGGTGCAGAGCTGGAGGAGGACATTGGCTCTCAAGGACCTGGCG	765		
DB	893	CTGAGCTTTGGAGCAGAGGGTGTGGTAATTACACGAACCTTGGCTCAAAAGACCAAGTCC	952		
QY	766	ATGCTCACTTGGAGCAGAAAGGTTTGGAGATGGAGGCAATCCACTACGATGGGTCTTC	825		
DB	953	CTGGCAAGCTTGGACACAGCTCTGCCACTCATGGAGGAGGCATCCCTTTGATGTACTTTTC	1012		
QY	826	ATCTGGAAGATCTCAGACTTGGCCAGGAAAGCTCCAGGAAGCTGTGGCTGGCCGCATACCC	885		
DB	1013	CTGTGGAAGATCAACCAATGTCAACAGCGGTGCCACGAGTCAGTGTGTGSCCGGACTGTC	1072		
QY	986	GCCATCTTCTCCCAAGCTTTCTACACAGCAGGTACGGGTACAAGATGTTCTTCGCGTATC	945		
DB	1073	AGCCTCTTCTTCAGCTTTTCTACTGCCAAGTATGGTTACAAGTTGTGCTTCGCGCTTG	1132		
QY	946	TACCTGAACGGCAGCGCACCGGCGAGGAACACACCTGTCCCTCTCTTTTGTGGTCAATG	1005		
DB	1133	TACCTGAACGGGATGGCTCAGGCAAGAACCCACCTGTCCCTCTTCATCGTATCATG	1192		
QY	1006	AAGGGCCGAATGACGCCCTCTGCGGTGGCCCTTCAACGAGAAGGTGACCTTAATGCTG	1065		
DB	1193	AGAGGAAATACGATGTCTCTCTCCCTGGCCTTTTCAGGAACAGAGTCACTTTATGCTTA	1252		

Query Match 21.4%: Score 272: DB 2: Length 2088;

Query Match 21.4%; Score 272; DB 2; Length 2088;

Best Local Similarity 63.8%; Pred. No. 5.5e-58;

Matches 429; Conservative 0; Mismatches 240; Indels

586 CTGGAGAAGACGGCCACTTTTGAGAACATTGTCTGCGTCTGAAACCGG

b 773 CTGGAGGAGAAGCTGCGTGTGTTTGCAACATTTGCTGTCTCAACAAG

2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526

646 AGGGTGGCCATGACTGCGGAGGCCCTGCAGCCGGCAGCACCTGGACCA

C
C
C
E
C
C
C
E
C
C
C
E
C
C
C
C
C
C
C
C
C
C
C
C

b
833 GCCTCCACCTGGCACTGGCCGCTCCATCCACAGAGCCAGTGGACCGG

705 CACCCCTGAGTACCAAGCTGCACGACGCTGGAGAGGAGCA TTGGCCCTCAAG

Y
708 GAAGCCCTGAGTAAACATGGTCAGCAGCCTGGAGAGAGAGCAATCGCCCTGCTTT

893 CTGAGCTTGGAGCGAGGGTGGTGGAAATTACAGCAACCCCTGGCTCAAAA

[illegible]

766 ATGGCTGACTTGGAGCAGAAGGTCTTGAGATGGAGGCATCCACCTACGAT

100

b
953 CTGGCAAGCTTGAGCACAGTCTGCGACTCATGGAGGAGGCATCCTTTGAT

826 ATCTGGAAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGTGGCTGGC

[illegible]

b 1013 CTGTGGAAGATCACCAATGTCAACCAAGCGGTGCCACGAGTCAGTGTGTGGC

[illegible]

886 GCCATCTTCTCCCCAGCCTTCTACACCCAGCAGGTACGGCTACAAGAAGTGGT

1073 AGCTTCTCTCCACGTTCTACATGCCAAGTATGGTACAAGTTGTGC

10/3 AGCCCTCTTCTCTCCAGCTTCTACACACGCGCCACAGATGGTACCAATTTGTG

946 TACCTGAACGGCGACGGCACCGGGCGAGGAACACACCTGTCCCTCTTCTTT

548

1133 TACCTGAACGGGGATGGCTCAGGCAAGAGACCCACCTGTCCCTCTTCTCATC

A

1006 AAGGGCCGAATGACGCCCTGCTGCCGTGGCCCTTCAACCAGAAAGGTGAC

10

1193 AGAGGAGAAATACGATGCTCTCCTGCCCTGGCCTTTTCAGGAACAAGGTCACCG

Qy	1066	CTCGACCCAGATTAACCGGAGACCGTGAATTGACGCTTTCAGGCCGACGTCATTC	1125
Db	1253	CTTGACCAAGAACACCGAGAGCATGCTATTGATGCTTCCGGCCTGACCTGAGCTCAGCC	1312
Qy	1126	TCTTTTTCAGAGGCCAGTCAACGACATGAACATCGCAGCGGCTGCCCTCTTCTGCCCC	1185
Db	1313	TCCTTCCAGCGGCCACAGAGTGAGACCAACGTGGCCAGCGGCTGCTCTTCTTCCCC	1372
Qy	1186	GTCTCCAGATGGAGGCA---AAGAAATTCCTACGTGCGGAGCAGTGCCATCTTCATCAAG	1242
Db	1373	CTCAGCAAGCTGCACTCACCAGCAGCGCTACGTCAAGATGACACAATGTTCTCTCAA	1432
Qy	1243	GCCATTGTGGAC	1254
Db	1433	TGCATTGTGGAC	1444

Search completed: November 6, 2004, 23:33:36
 Job time : 134 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 20:48:57 ; Search time 701 Seconds
(without alignments)
9746.709 Million cell updates/sec

Title: US-10-018-030B-1
Perfect score: 1269
Sequence: 1 atggctgcagctagcgtgac.....tggacctgacagggctctaa 1269

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 262057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	959.6	75.6	1506	US-10-361-270-2	Sequence 2, Appli
2	959.6	75.6	2262	US-09-962-832-121	Sequence 121, Appl
3	959.6	75.6	2262	US-09-954-456-1186	Sequence 1186, Ap
4	959.6	75.6	2262	US-10-067-125-2	Sequence 2, Appli
5	855.6	67.4	2094	US-10-094-749-63	Sequence 63, Appl
6	701	55.2	2121	US-10-283-500-3	Sequence 3, Appli
7	236.6	23.4	1251	US-10-085-117-330	Sequence 330, App
8	236.6	23.4	2380	US-10-067-125-1	Sequence 1, Appli
9	236.6	23.4	2380	US-10-172-118-1184	Sequence 1184, Ap
10	236.6	23.4	2380	US-10-085-117-329	Sequence 329, App
11	236.6	23.4	2380	US-10-342-887-1184	Sequence 1184, Ap
12	236.6	23.4	5981	US-10-044-090-823	Sequence 823, App

13	276.8	21.8	2361	15	US-10-453-478-7	Sequence 7, Appli
14	272	21.4	481	10	US-09-918-995-28886	Sequence 28886, A
15	272	21.4	1230	15	US-10-085-117-327	Sequence 327, App
16	272	21.4	2088	15	US-10-283-500-1	Sequence 1, Appli
17	272	21.4	2088	15	US-10-085-117-326	Sequence 326, App
18	190.8	15.0	354	9	US-09-796-692-5702	Sequence 5702, Ap
19	190.8	15.0	354	14	US-10-040-862-5702	Sequence 5702, Ap
20	190.8	15.0	354	16	US-10-057-475B-5702	Sequence 5702, Ap
21	190.8	15.0	354	16	US-10-154-884B-5702	Sequence 5702, Ap
22	190.8	15.0	354	17	US-10-764-324-5702	Sequence 5702, Ap
23	189.2	14.9	354	9	US-09-796-692-5613	Sequence 5613, Ap
24	189.2	14.9	354	14	US-10-040-862-5613	Sequence 5613, Ap
25	189.2	14.9	354	16	US-10-057-475B-5613	Sequence 5613, Ap
26	189.2	14.9	354	16	US-10-154-884B-5613	Sequence 5613, Ap
27	189.2	14.9	354	17	US-10-764-324-5613	Sequence 5613, Ap
28	171.6	13.5	1581	16	US-10-262-445-129	Sequence 129, App
29	171.6	13.5	1661	16	US-10-042-865-49	Sequence 49, Appl
30	171.6	13.5	1707	16	US-10-262-445-131	Sequence 131, Appl
31	171.6	13.5	1787	16	US-10-042-865-37	Sequence 37, Appl
32	171.6	13.5	2738	11	US-09-968-007A-803	Sequence 803, App
33	171.6	13.5	3480	15	US-10-004-378A-3	Sequence 3, Appli
34	171.6	13.5	3675	15	US-10-004-378A-1	Sequence 1, Appli
35	171.6	13.5	3993	14	US-10-067-125-5	Sequence 5, Appli
36	171.6	13.5	3993	15	US-10-172-118-2	Sequence 2, Appli
37	171.6	13.5	3993	16	US-10-342-887-2	Sequence 2, Appli
38	151.8	12.0	2359	8	US-08-813-323A-3	Sequence 3, Appli
39	146.6	11.6	1792	9	US-09-950-902-3	Sequence 3, Appli
40	146.6	11.6	2240	9	US-10-342-212-6	Sequence 1, Appli
41	146.6	11.6	2339	14	US-10-207-655-102	Sequence 102, App
42	146.6	11.6	2065	9	US-09-950-902-1	Sequence 1, Appli
43	145	11.4	2455	8	US-08-813-323A-4	Sequence 4, Appli
44	145	11.4	2455	14	US-10-067-125-3	Sequence 3, Appli
45	145	11.4	2455	14	US-10-067-125-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-361-270-2
; Sequence 2, Application US/10361270
; Publication No. US20040038299A1
; GENERAL INFORMATION:
; APPLICANT: Kuai, Jun
; APPLICANT: Wooters, Joseph L
; APPLICANT: Nickbarg, Elliott
; APPLICANT: Qiu, Yongchang
; APPLICANT: Lin, Lin-Ling
; TITLE OF INVENTION: Composition and Method for Modulating an Inflammatory
; FILE REFERENCE: 22058-565
; CURRENT APPLICATION NUMBER: US/10/361,270
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/355,183
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-270-2

Query Match 75.6%; Score 959.6; DB 16; Length 1506;
Best Local Similarity 81.7%; Pred. No. 7.5e-271;
Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;

QY	1	ATGGCTGCAGCTAGCTGACCCCTGGCTCCCTGGAGTTGCTACACGCCGGCTTCTCC	60
DB	1	ATGGCTGCAGCTAGCTGACCCCTGGCTCCCTGGAGTTGCTACACGCCGGCTTCTCC	60
QY	61	AAAGACCTCTGGGACCAAGCTGGAAGCAAGTGTGTGCTCGCTGCAGAACGTC	120

Dd		61	AAGACCTCCTCGGGACCAGCTGGAAGCCAAAGTACTGTGCTCCGCCCTGCAGAAAACGTC	121
Qy		121	CTCCGCAAGCCCCTTCACGCGCAGTGTTGGCCACACCGGTACTGCTCTCTTCTGCTCTGCACGC	180
Dd		121	CTCCGCAAGCCCCTTCACGCGCAGTGTTGGCCACACCGGTACTGCTCTCTTCTGCTCTGCACGC	180
Qy		181	ATCCTCAGCTCTGGGCTCAGAACTGTGCTGCTCTGTGTTTACGAGGGCATATATGAAGA	240
Dd		181	ATCCTCAGCTCTGGGCTCAGAACTGTGCTGCTCTGTGTTTACGAGGGCATATATGAAGA	240
Qy		241	GCGATTCTTAATTTAGAAAGCAGTTCGCGCTTCCAGATAATCTCTCCCGCAGGAGGTG	300
Dd		241	GCGATTCTTAATTTAGAAAGCAGTTCGCGCTTCCAGATAATCTCTCCCGCAGGAGGTG	300
Qy		301	GAGAGCTGCGCGCGCTGTCTCCAGTGATGATGCACTTGAAGGGGACCTGTAAGA	360
Dd		301	GAGAGCTGCGCGCGCTGTCTCCAGTGATGATGCACTTGAAGGGGACCTGTAAGA	360
Qy		361	TACG-----	361
Dd		361	TACGAGAGCTGCACAGAGCGCTGCCCGCTCATGCTGACCGAATGTCCCCGCTGTAAA	420
Qy		365	-----	364
Dd		421	GCGCTGCTCGCCTTGTTGTAAGAGAGCGCCA CTGGAGCACGAGTGC CGGAGAGA GC	480
Qy		365	-----	364
Dd		481	CTGAGCTGCGCGCATATGCGCGGCACCCCTGTGCGBAGCAGACGTGAA GCGCAC CACGAG	540
Qy		365	-----	364
Dd		541	GTCTGCCCAAAGTTCCCTTAACTTTGTGACGGCTGCGGCAAGAAGAAGATCCCCCGGAG	600
Qy		365	-AGTTTCAGGACCAAGTCCAGACA CTTGTGGCAAGTGTCTGAGTCCCTTG CAGATTCACGCC	423
Dd		601	AAGTTTCAGGACCAAGTCCAGACA CTTGTGGCAAGTGTCTGAGTCCCTTG CAGATTCACGCC	660
Qy		424	ATCGGCTGCCCTCAGAGCGCTAGAGGGTGAAAAACGACGAGGACGACGAGTGCAGTGGCGTG	483
Dd		661	ATCGGCTGCCCTCAGAGCGCTAGAGGGTGAAAAACGACGAGGACGACGAGTGCAGTGGCGTG	720
Qy		484	CGGAGACACTTGGCCATGCTACTGAGTCTGGTCTGGAGCGAAAAAGCCCTCTTGGAGAC	543
Dd		721	CGGAGACACTTGGCCATGCTACTGAGTCTGGTCTGGAGCGAAAAAGCCCTCTTGGAGAC	780
Qy		544	CAGAGCCACGCGGGTTCAGAGCTCCTGCAAGTGTGAGAGCCTCGAGAGAACGAGC	603
Dd		781	CAGAGCCACGCGGGTTCAGAGCTCCTGCAAGTGTGAGAGCCTCGAGAGAACGAGC	840
Qy		604	ACTTTTGAGAACATTTGCTCGTCTGAACCGGAGGTGGAGAGGTCGCCATGACTGCC	663
Dd		841	ACTTTTGAGAACATTTGCTCGTCTGAACCGGAGGTGGAGAGGTCGCCATGACTGCC	900
Qy		664	GAGGCTTCGACCGGACGACCGCTGGACCAAGACAGATTGAAGCCCTGAGTAGCAG	723
Dd		901	GAGGCTTCGACCGGACGACCGCTGGACCAAGACAGATTGAAGCCCTGAGTAGCAG	960
Qy		724	GTGACGAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGGCGATGGCTGACTTGGAGCAG	783
Dd		961	GTGACGAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGGCGATGGCTGACTTGGAGCAG	1020
Qy		784	AAGTCTTTGNATGAGAGGCATCCACTAGCATGGGTCTTCATCTGGAAGATCTCAGAC	843
Dd		1021	AAGTCTAGGCGCCTTCCAGGCGGAGTGTGGCCACCGGTACTGTCTCTTGTGCTGCGCCAGC	1080
Qy		844	TTCCGCCAGGAAGCTTCCAGGAAGCTGTGGCTGGCGCGCATACCGCGCATCTTCTCCCGCAGCC	903
Dd		1081	ATCCTCAGGAAGCTCCAGGAGCTGTGGCTGTGSCCGCATACCGCGCATCTTCTCCCGCAGCC	1140
Qy		904	TTCTACACGAGAGGTACGGCTACAGATGTGTGTGCGGTATCTACCTGAACGGCGCAGCGG	963
Dd		1141	TTCTACACGAGAGGTACGGCTACAGATGTGTGTGCGGTATCTACCTGAACGGCGCAGCGG	1200

RESULT 2

RESULT 2
US-09-962-832-121
; Sequence 121, Application US/09962832

; Patent No. US20020110821A1
: GENERAL INFORMATION:

```

; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatur

```

; TITLE OF INVENTION: Sets
: FILE REFERENCE: 689290-74

FILE REFERENCE: 683250-74
CURRENT APPLICATION NUMBER: US/O

; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/2335-077

PRIOR FILING DATE: 2000-09-25

; PRIOR APPLICATION NUMBER: US/6
: PRIOR FILING DATE: 2000-09-25

; FROM FILING
; NUMBER OF SEQ

```

; SOFTWARE: Pat
; SEQ ID NO 121

```

; SEQ ID NO 121
; LENGTH: 2262

```

; TYPE: DNA
; ORGANS: Hom

```

Query Match 75.6%; Score 959.6; DB 9; Length 2262;
Best Local Similarity 81.7%; Pred. No. 8.4e-271;
Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;

1	ATGGCTGAGCTAGCTAGTGAACCCCCCTTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC	60
55	ATGGCTGAGCTAGCTAGTGAACCCCCCTTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC	114
61	AAGACCTCTCTGGGGACCAAGCTGGGAAGCAAGTACTCTGCTCCGCTCGCAGAAAGCTC	120
115	AAGACCTCTCTGGGGACCAAGCTGGGAAGCAAGTACTCTGCTCCGCTCGCAGAAAGCTC	174
121	CTCCGCAAGGCCCTTCCAGGCGCAGTGTGCCACCGGTACTGCTCTCTTGCTGGCCGAGC	180
175	CTCCGCAAGGCCCTTCCAGGCGCAGTGTGCCACCGGTACTGCTCTCTTGCTGGCCGAGC	234
181	ATCTCTGAGCTCTGGGCTCAGACTGCTGCTGCTGTTCCAGAGGGCATATATGAGAA	240
235	ATCTCTGAGCTCTGGGCTCAGAACTGTGCTGCTGTTCAGAGGGCATATATGAGAA	294
241	GGCATTTCTATTTAGAAAGCAAGTTCGGCCTTCCCAAGATAATGTCGCCCGCAGGAGGTG	300
295	GGCATTTCTATTTAGAAAGCAAGTTCGGCCTTCCCAAGATAATGTCGCCCGCAGGAGGTG	354

QY	365	-----	364
Db	475	GGCCTGGTCCGCTTGGTGAAGAGGAGCGCCACCTGGAGCAGAGTCCCGGAGAGAAC	534
QY	365	-----	364
Db	535	CTGAGCTCCGGCATTCGCGGCACCTGTGCGGAGCAGACGTGAAGGCGCACACGAG	594
QY	365	-----	364
Db	595	GTCTGCCCAAGTTCCCTTAACTTGTCAGCGGTGCGGCAAGAAGAGATCCCCCGGAG	654
QY	365	-AGTTTCAGGACCAAGTCAAGACTTTGGCAAGTTCGAGTCCCTTGACGANTTCCACGCC	423
Db	655	AAGTTTCAGGACCAAGTCAAGACTTTGGCAAGTTCGAGTCCCTTGACGANTTCCACGCC	714
QY	424	ATCCGCTCCTCGAGAGCGGTAGAGGGTGAAGAACAGCAGCAGGACGAGGTGCAGTGCCTG	483
Db	715	ATCCGCTCCTCGAGAGCGGTAGAGGGTGAAGAACAGCAGCAGGACGAGGTGCAGTGCCTG	774
QY	484	CGGAGCACCTGGCCATGCTACTCAGCTCGGTGTGAGGCAAGGCCCTCTTTGGGAGAC	543
Db	775	CGGAGCACCTGGCCATGCTACTCAGCTCGGTGTGAGGCAAGGCCCTCTTTGGGAGAC	834
QY	544	CAGAGCCACGGGGGTGAGACTCTCGAGAGGTCGAGAGCCTCGAGAGAGAGACGCGC	603
Db	835	CAGAGCCACGGGGGTGAGACTCTCGAGAGGTCGAGAGCCTCGAGAGAGAGACGCGC	894
QY	604	ACTTTTGAGAACATTGTCTGGTCTCTGAACCGGAGGTCGAGAGGTCGACATGACTGCC	663
Db	895	ACTTTTGAGAACATTGTCTGGTCTCTGAACCGGAGGTCGAGAGGTCGACATGACTGCC	954
QY	664	GAGGCTCAGCCGCGACGACCGGCTGGAACAGACAAAGATTGAAGCCCTGATAGCAAG	723
Db	955	GAGGCTCAGCCGCGACGACCGGCTGGAACAGACAAAGATTGAAGCCCTGATAGCAAG	1014
QY	724	GTGAGCAGCTGGAGAGAGCATTTGGCTCAAGACCTGCGATGGCTGACTTTGGAGCAG	783
Db	1015	GTGAGCAGCTGGAGAGAGCATTTGGCTCAAGACCTGCGATGGCTGACTTTGGAGCAG	1074
QY	784	AAGGCTTTGGAGATGGAGGCAATCCACTGATGGGTCTTCATCTGGAAGATCTCAGAC	843
Db	1075	AAGGTCAGGCCCTTCCAGGCGCAGTGTGGCCACCGGTACTGCTCTTCTGCTGGCCAGC	1134
QY	844	TTGCGCAGGAAGCTCCAGGAAGCTGTGGCTGCGCGCATACCGGCCATCTTCTCCCGACC	903
Db	1135	ATCCTTCAGGAAGCTCCAGGAAGCTGTGGCTGCGCGCATACCGGCCATCTTCTCCCGACC	1194
QY	904	TTCTACACAGCAGGTAGGCTCAAGATGTGTCTGGTATCTACCTGAACGGCGACGGC	963
Db	1195	TTCTACACAGCAGGTAGGCTCAAGATGTGTCTGGTATCTACCTGAACGGCGACGGC	1254
QY	964	ACCGGCGAGGAACACACTGTCCCTCTTTGTGTGATGAAGGCCCGAATGACGCC	1023
Db	1255	ACCGGCGAGGAACACACTGTCCCTCTTTGTGTGATGAAGGCCCGAATGACGCC	1314
QY	1024	CTGCTCGGTGCGCTTCAACAGAGAGTGACCTTAATGCTGCTCGACCAAGAAATACCGG	1083
Db	1315	CTGCTCGGTGCGCTTCAACAGAGAGTGACCTTAATGCTGCTCGACCAAGAAATACCGG	1374
QY	1084	GAGCAGTGATTTAGCGCTTTCAGGCGCGACGTGACTTCATCCTCTTTTCAGAGGCCAGTC	1143
Db	1375	GAGCAGTGATTTAGCGCTTTCAGGCGCGACGTGACTTCATCCTCTTTTCAGAGGCCAGTC	1434
QY	1144	AACGACATGAACATGCAAGGGCTGCCCTCTTCTGCCCGCTCTCCAGATGGAGCA	1203
Db	1435	AACGACATGAACATGCAAGGGCTGCCCTCTTCTGCCCGCTCTCCAGATGGAGCA	1494
QY	1204	AAGAAATTCCTAGTGGGGACGATGCCATCTTCATCAAGGCCATTGTGGACCTGACAGGG	1263
Db	1495	AAGAAATTCCTAGTGGGGACGATGCCATCTTCATCAAGGCCATTGTGGACCTGACAGGG	1554

Qy	1264	CTCTAA	1269	
Db	1555	CTCTAA	1560	
RESULT 5				
US-10-094-749-63				
; Sequence 63, Application US/10094749				
; Publication No. US2003021974A1				
; GENERAL INFORMATION:				
; APPLICANT: ISOGAI, TAKAO				
; APPLICANT: SUGIYAMA, TOMOYASU				
; APPLICANT: OTSUKI, TETSUJI				
; APPLICANT: WAKAMATSU, AI				
; APPLICANT: SATO, HIROYUKI				
; APPLICANT: ISHII, SHIZUKO				
; APPLICANT: YAMAMOTO, JUN-ICHI				
; APPLICANT: ISONO, YUUKO				
; APPLICANT: HIO, YURI				
; APPLICANT: OTSUKA, KAORU				
; APPLICANT: NAGAI, KEIICHI				
; APPLICANT: IRIE, RYOTARO				
; APPLICANT: TAMECHIKA, ICHIRO				
; APPLICANT: SEKI, NAOHICO				
; APPLICANT: YOSHIKAWA, TSUTOMU				
; APPLICANT: OTSUKA, MOTOUYUKI				
; APPLICANT: NAGAHARI, KENJI				
; APPLICANT: MASUHO, YASUHIKO				
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA				
; FILE REFERENCE: 084335/0160				
; CURRENT APPLICATION NUMBER: US/10/094,749				
; PRIOR FILING DATE: 2002-03-12				
; PRIOR APPLICATION NUMBER: 60/350,435				
; PRIOR FILING DATE: 2002-01-24				
; PRIOR APPLICATION NUMBER: JP 2001-328381				
; PRIOR FILING DATE: 2001-09-14				
; NUMBER OF SEQ ID NOS: 3381				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 63				
; LENGTH: 2094				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-094-749-63				
Query Match 67.4%; Score 855.6; DB 15; Length 2094;				
Best Local Similarity 81.5%; Pred. No. 2.6e-240;				
Matches 1095; Conservative 0; Mismatches 174; Indels 75; Gaps 6				
Qy	1	ATGCTGCAGCTAGCGTGACCCCGCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCCTCC	60	
Db	45	ATGCTGCAGCTAGCGTGACCCCGCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCCTCC	104	
Qy	61	AAGACCCCTCCTGGGACCAAGCTGGAAAGCAAGTACCTGTGCTCCGCTGCAGAAACGTC	120	
Db	105	AAGACCCCTCCTGGGACCAAGCTGGAAAGCAAGTACCTGTGCTCCGCTGCAGAAACGTC	164	
Qy	121	CTCCGACGGCCCTTCACGGCCGAGTGTGGCCACCGGTACTGCTCCTCTGCTGGCCAGC	180	
Db	165	CTCCGACGGCCCTTCACGGCCGAGTGTGGCCACCGGTACTGCTCCTCTGCTGGCCAGC	224	
Qy	181	ATCCTCAGCTCTGGGCCCTCAGAACTGTGCTGCCTGTGTTACAGGGGCATATATGAAGAA	240	
Db	225	ATCCTCAGCTCTGGGCCCTCAGAACTGTGCTGCCTGTGTTACAGGGGCATATATGAAGAA	284	
Qy	241	GGCATTTCTATTTTAGAAGAGTTTCGCCCTTCCCAAGATAATGCTGCCCGCAGGGAGGTG	300	
Db	285	GGCATTTCTATTTTAGAAGAGTTTCGCCCTTCCCAAGATAATGCTGCCCGCAGGGAGGTG	344	
Qy	301	GAGAGCCTGCCGGCCGCTGTGTCACAGTCATGATGCACCTGGAAGGGGACCCCTGAAAGAA	360	
Db	345	GAGAGCCTGCCGGCCGCTGTGTCACAGTCATGATGCACCTGGAAGGGGACCCCTGAAAGAA	404	
Qy	361	TACGAGTTTCA-----GGACCACGTCAGACCTTGTGGCAAGTGTGAGTCCCTTT	409	

Db 468 GGCCTGGTCCGCTCAGCGAGGAGGAGCACCACACTGACGAGGATGCCCAAAAGGAGC 527
 QY 366 ----- 365
 Db 528 CTGAGCTGCCAGCACTGCGAGCACCCCTGTAGCCAGTGGACCTGGAGGTACACTATGAG 587
 QY 366 ----- 365
 Db 588 GTCTGCCCAAGTTTCCCTTAACCTGTGATGCTGTGGCAAGAGAGATCCCTCGGGAG 647
 QY 366 --GTTTCAGAGCACCTCAAGACTTGTGGCAAGTGTGAGTGCCTTTCAGATTCACAGCC 423
 Db 648 ACCTTTTCAGAGCACTTGTAGAGCATGCAAGAAATGCCGGTTCTCTGCAAGTTCACACC 707
 QY 424 ATCGGCTGCTCGAGAGCTGAGGCTGAGAACACAGAGAGAGAGAGTGCAGTGGCTG 483
 Db 708 GTTGGCTGTTTCAGAGATGTTGAGACTGAGAACCTGAGGATCATGAGTGCAGCGGCTA 767
 QY 484 CGGAGCACTGCGCACTGCTACTGAGCTCGTGTGAGGCAAGCCCTCTTTGGAGAGAC 543
 Db 768 CGGGAACACTAGCCCTACTGCTGAGCTCATCTTGGAGGCCCAAGCTCTCCAGGAGCC 827
 QY 544 CAGAGCAGCGGGGTGAGAGCTCTGAGAGAGTGGAGAGCTGGAGAGAGAGAGAGAGAGC 603
 Db 828 TTGAACAGGTGGGGCCAGAGCTACTCCAGCGGTGCCAGATTTTGAGAGAGAGATAGCA 887
 QY 604 ACTTTTGAAGAACTTCTCGCTCTGAAACCGGAGGTGAGAGGTTGCCATGACTGCC 663
 Db 888 ACCTTTGAGAACATTTCTGCGTCTTGAACCTGAGTGAAGTAGAGGTTGAGTGAAGTGA 947
 QY 664 GAGGCTGAGCGGCGAGCAGCCGCTGGAACCAAGAACAGATTGAAGCCCTGAGTAGCAAG 723
 Db 948 GAGGCTTGTAGCGGCGAGCAGCCGCTGAGACAGGACCAAGATTGAGGCCCTGAGTAACA 1007
 QY 724 GTGCAGAGCTGAGAGAGAGATGCGCTCAAGGACCTGCGATGCTGACTTGGAGGAG 783
 Db 1008 GTGCAGAGCTGAGAGAGAGATGCGCTCAAGGACCTGCGATGCTGACTTGGAGGAG 1067
 QY 784 AAGGCTTGGAGATGAGGAGCATCCACTACGATGGGCTTTCATCTGGAAGATCTCAGAC 843
 Db 1068 AAGGCTCCGAGTTGGAAGTATCCACTATGATGGGCTTTCATCTGGAAGATCTCAGAC 1127
 QY 844 TTGCGCAGAGAGCTCCAGAGAGTGTGGCTGGCGCATACCCGCCATCTTCTCCCGAGCC 903
 Db 1128 TTACACAGAAAGCGTCAGAGAGCGTGTGCTGGCGGACACCAAGCTATCTTCTCCCGAGCC 1187
 QY 904 TTCTACACAGAGTACCGGCTACAGAGATGTGTCTGCGTATCTACTGAAACCGGACCGCC 963
 Db 1188 TTCTACACAGAGATAGGCTACAGATGTGTCTACGAGTCTACTTGAATGGCGAGCGC 1247
 QY 964 ACCGGCGAGGAGAACACACCTGTCTCTTTTGTGGTGTATGAAGGCCCGGATGACGCC 1023
 Db 1248 ACTGGCGGGGAACTCATCTGTCTCTTCTTCTGTTGATGAAAGGCCCAATGATGCT 1307
 QY 1024 CTGCTCGGTGGCCCTTCAACAGAGGTGACCTTAATGCTGCTGACACAGATTAACCGG 1083
 Db 1308 CTGTTGAGTGGCTTTTAACTGAAAGGTAAATGATGTTGCTGACCATTAACACCGG 1367
 QY 1084 GAGCAGTGTATGAGCCCTTCAGGCCCGGAGCTGACTTCACTCTTTTCAGAGGCCAGTGC 1143
 Db 1368 GAGCAGTGTATGAGCCATTCAGGCCCGGATGAACCTGCTCTCTTTCAGAGGCCCTGTC 1427
 QY 1144 AACGACATGAACTCCAGAGCGGCTGCGCCCTCTTCTGCGCCGCTCTCCAGAGTGAAGCA 1203
 Db 1428 AGTGACATGAACATCGCCAGTGGCTGCGCCCTCTTCTGCGCCCTGTGTCCAGATGAGGCC 1487
 QY 1204 AAGAAATTCCTACGTGGGAGCAGATGCCATCTTTCATCAAGGCCATGTGGACCTGACAGG 1263
 Db 1488 AAGAAATTCCTACGTGGGAGTATGAGATCTTTCATCAAGGCTATGTGGACCTTACAGGA 1547
 QY 1264 CTCTA 1268
 |||||

Db 1548 CTCTA 1552
 RESULT 7
 US-10-085-117-330
 ; Sequence 330, Application US/10085117
 ; Publication No. US2003023234A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris David W.
 ; APPLICANT: Engelhard, Eric K.
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 ; FILE REFERENCE: 529452000121
 ; CURRENT APPLICATION NUMBER: US/10/085,117
 ; PRIOR FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: US 09/799,586
 ; NUMBER OF SEQ ID NOS: 361
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 330
 ; LENGTH: 1251
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-085-117-330
 Query Match 23.4%; Score 296.6; DB 15; Length 1251;
 Best Local Similarity 66.2%; Pred. No. 2.1e-76;
 Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;
 QY 586 CTGAGAGAGAGAGCGCCACTTTTGGAGAACATTTCTCGCTCTGAAACCGGAGGTGGAG 645
 Db 568 CTGAGGGGAAGCTGCGTGTGTTTGGAGAACATTTGCTGTCTTCAACAAAGGAGGTGGAG 627
 QY 646 AGGTTGCCATGACTGCGAGGCTGCAGCGGCGAGCAGCCGGTGGAGCCCAAGAGATT 705
 Db 628 GCCTCCACCTGGCCCTGGCCACCTCTATCCACAGAGCCAGCTGGACCGTGGAGCGCATC 687
 QY 706 GAAGCCCTGAGTAGCAAGGTGCAGCAGTGGAGAGAGCATTTGGCCTCAAGGACCTGGCG 765
 Db 688 CTGAGCTTGGAGCAGAGGCTTGGAGCTTCAGCAGACCCCTGGGCCAAGAACACCGGCC 747
 QY 766 ATGCTGACTTGGAGCAGAGAGGCTTTGGAGATGGAGGATCCACCTACGATGGGCTTTC 825
 Db 748 CTGGCAAGCTGGAGCAGAGAGCTTGGCCCTCATGGAGGAGGCTCTTCGATGGACATTC 807
 QY 826 ATCTGGAAGATCTCAGACTTTCGCGCAGGAAGCTCCAGAAAGCTGTGGCTGGCGGATACCC 885
 Db 808 CTGTGAAGATCAACAAATGTACCCAGCGGTGCCATGAGTCCGCTGTGGCAGGACCGTC 867
 QY 886 GCCATCTTCCCGCAGCCTTCTACACAGCAGAGTACGCGCTACAAGATGTGTCTGCGTATC 945
 Db 868 AGCTCTTCTCCCGCAGCCTTCTACCTGCGCAAGTATGGCTAAGTTGTGCTGCGGCTG 927
 QY 946 TACTGAACCGCGCAGCGCACCGGCGAGGAAACACACTGTCCCTCTTCTTTTGGTGGATG 1005
 Db 928 TACCTGAATGGAGATGGCACTGGAAAGAGAAACCACTGTGCGCTCTTCATCGTATCATG 987
 QY 1006 AAGGGCCGATGAGCCCTGCTGCGGTGGCCCTTCAACAGAGAGTGAACCTTAATGCTG 1065
 Db 988 AAGGGGAGTATGATGCGCTGCTGCGGTGGCCCTTCCGGAACCAAGGTCACTTCATGCTG 1047
 QY 1066 CTCACACAGAAATACCGGAGCAGCTGATTTGAGCGCTTCAGGGCCGACGCTGACTTCATCC 1125
 Db 1048 CTGACCCAGAACACCTGAGCAGCGCCATTTGACGCTTCCGGCCTGACCTAAGCTCAGCG 1107
 QY 1126 TCTTTTCAGAGGCGAGTCAACGACATGAACATGCAAGAGGCTGCCCGCTCTTCTGCCCC 1185
 Db 1108 TCTTCCAGAGGCCCCCAAGAGTGAACCAACAGTGGCAGTGGATGCCACCTCTTCTTCCCC 1167
 QY 1186 GTCTCCAAAGTGGAGGCA---AAGAAATCTTACGTGGCGGACGATGCCATCTTTCATCAAG 1242
 Db 1168 CTAGCAAACTGCACTACCCAGCAAGCGCTACGTGAAGGACGACAAATGTTCTTCTCAAG 1227
 QY 1243 GCCATTGTGGA 1253

Db 1228 TGCATTGTGGA 1238

RESULT 8

US-10-067-125-1
; Sequence 1, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowser, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 1
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1326)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: U19261 Genbank
; DATABASE ENTRY DATE: 1995-02-21
US-10-067-125-1

Query Match 23.4%; Score 296.6; DB 14; Length 2380;
Best Local Similarity 66.2%; Pred. No. 2.5e-76;
Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

QY 586 CTGGAGAGAAAGACGGCCACTTTTGAACAATTTCTGCGTCTTGAACCGGGAGGTGGAG 645
Db 643 CTGGAGGGGAAAGTCGCTGTGTTTGAACAATTTCTGCTCTCAACAAGGAGGTGGAG 702
QY 646 AGGCTGGCCATGACCTGCGGAGGCTGAGCGGCGGAGCAGCGGCTGGACCAAGCAAGATT 705
Db 703 GCCTCCCACTTGGCCCTGCGCCACTCTATCCAGAGCGAGCTGGACCGTGGAGCGCATC 762
QY 706 GAAGCCCTGAGTAGCAAGGTGACAGCTGGAGAGGAGCATTTGGCCCTCAAGGACCTGGCG 765
Db 763 CTGAGCTTGGAGCAGAGGGTGGTGGAGCTTCAGCAGACCTTGGCCCGCAGAAAGACCGCC 822
QY 766 ATGGCTGACTTGGAGCAGAGGCTTGGAGATGGAGGATCCACCTACGATGGGGTCTTC 825
Db 823 CTGGGCAAGCTGGAGCAGAGCTTGGCCCTATGAGGAGGCGCTCTTCGATGGGACTTTC 882
QY 826 ATCTGGAAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGGCTGGCCGATACCC 885
Db 883 CTGTGGAAGATCACCATGTCCACGCGGCTGGTGGAGCTTCAGCAGACCTTGGCCCGCAG 942
QY 886 GCGATCTTCTCCCGAGCTTCAACAGCAGGTACGGCTTCAAGATGTGTCTGCGTATC 945
Db 943 AGCCTCTTCTCCCGAGCTTCACTGCGCAAGTATGGCTTCAAGTGTGCTGCGGCTG 1002
QY 946 TACTGGAACGCGGAGCGGCGGAGGACACACTGCTCCCTCTTCTTTTGTGTGATG 1005
Db 1003 TACTGGAATGGAGATGGCATGGGAAGAGAACCCATCTGTCTTCTTCATCGTATCATG 1062
QY 1006 AAGGCGCGAATAGCGCCCTGCTCGGTGGCCCTTCAACAGAGGTGACCTTAATGCTG 1065
Db 1063 AGAGGGAGTATGATGCTGCTGCGCTGGCCCTTCCGGAACAGGTGACCTTCATGCTG 1122
QY 1066 CTCGACAGATACCGGAGCAGCTGATTTGAGCGCTTCAGGCCCGCAGCTTCAATCC 1125
Db 1123 CTGACCAAGAACACCGTGAGCAGCCATTGACCGCTTCGGGCTGACCTTAAGCTAGCG 1182
QY 1126 TCTTTTTCAGAGGCCAGTCAACGACATGAACATCGAAGCGGCTGCCCCCTCTTCTGCCCC 1185

Db 1183 TCCTTCCAGAGGCCCCAGAGTGAAACCAACGTGGCCAGTGATGCCACTCTTCTTCCCC 1242
QY 1186 GTCTCAAGATGGAGGCA---AAGAAATTCCTACGTGCGGGAGCATGCCATCTTCAATCAAG 1242
Db 1243 CTGAGCAAACTGCAGTCCACCAAGCAGCCTACGTGAAGGAGCAGACAAATGTTCTCTCAAG 1302
QY 1243 GCATTGTGGA 1253
Db 1303 TGCATTGTGGA 1313

RESULT 9

US-10-172-118-1184
; Sequence 1184, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1184
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005658
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1184

Query Match 23.4%; Score 296.6; DB 15; Length 2380;
Best Local Similarity 66.2%; Pred. No. 2.5e-76;
Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;
QY 586 CTGGAGAGAAAGACGGCCACTTTTGAACAATTTCTGCGTCTTGAACCGGGAGGTGGAG 645
Db 643 CTGGAGGGGAGCTGCGTGTGTTTGAACAATTTGTTGCTGCTCTCAACAAGGAGGTGGAG 702
QY 646 AGGCTGGCCATGACCTGCGGAGGCTGAGCGGCGGAGCAGCGGCTGGACCAAGCAAGATT 705
Db 703 GCCTCCCACTTGGCCCTGCGCCACTCTATCCAGAGCGAGCTGGACCGTGGAGCGCATC 762
QY 706 GAAGCCCTGAGTAGCAAGGTGACAGCTGGAGAGGAGCATTTGGCCCTCAAGGACCTGGCG 765
Db 763 CTGAGCTTGGAGCAGAGGGTGGTGGAGCTTCAGCAGACCTTGGCCCGCAGAAAGACCGCC 822
QY 766 ATGGCTGACTTGGAGCAGAGGCTTGGAGATGGAGGATCCACCTACGATGGGGTCTTC 825
Db 823 CTGGGCAAGCTGGAGCAGAGCTTGGCCCTATGAGGAGGCGCTCTTCGATGGGACTTTC 882
QY 826 ATCTGGAAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGGCTGGCCGATACCC 885
Db 883 CTGTGGAAGATCACCATGTCCACGCGGCTGGTGGAGCTTCAGCAGACCTTGGCCCGCAG 942
QY 886 GCGATCTTCTCCCGAGCTTCTTACACGAGGAGTACGGCTTCAAGATGTGTCTGCGTATC 945
Db 943 AGCCTCTTCTCCCGAGCTTCTTACACTGCGCAAGTATGGCTTCAAGTGTGCTGCGGCTG 1002
QY 946 TACTGGAACGCGGAGCGGCGGAGGACACACTGCTCCCTCTTCTTTTGTGTGATG 1005
Db 1003 TACTGGAATGGAGATGGCATGGGAAGAGAACCCATCTGTCTTCTTCATCGTATCATG 1062
QY 1006 AAGGCGCGAATAGCGCCCTGCTCGGTGGCCCTTCAACAGAGGTGACCTTAATGCTG 1065
Db 1063 AGAGGGAGTATGATGCTGCTGCGCTGGCCCTTCCGGAACAGGTGACCTTCATGCTG 1122
QY 1066 CTCGACAGATACCGGAGCAGCTGATTTGAGCGCTTCAGGCCCGCAGCTTCAATCC 1125
Db 1123 CTGACCAAGAACACCGTGAGCAGCCATTGACCGCTTCGGGCTGACCTTAAGCTAGCG 1182
QY 1003 TACCTGGAATGGAGATGGCAGCTGGAAAGAGAACCCACTCTGTGCTCTTCACTGATCATG 1062

QY 1006 AAGGCCCCGAATGACGCCCTGCTGGTGGCCCTTCAACCAAGAGTGACCTTAATGCTG 1065
 Db 1063 AGAGGGAGTATGATGCGTGTGCGCTGGCCCTTCCGGAACAAGGTACCTTCAATGCTG 1122
 QY 1066 CTGACCCAGAAATACCGGGAGACGCTGATTGAGCCCTTCAGGCCCCAGCGTCACTTCATCC 1125
 Db 1123 CTGACCCAGAAACAACCGTGAGCAGCCATTGACGCCCTTCGGCCCTGACCTAAGCTCAGG 1182
 QY 1126 TCTTTTCAGAGGCCAGTCAACGACATGACATCGCAAGCGGCTGCCCCCTCTTCTGCCCC 1185
 Db 1183 TCCTTCCAGAGGCCAGAGTGAACCAACGTTGGCCAGTGGATGCCCACTCTTCTTCCCC 1242
 QY 1186 GTCTCCAAAGATGAGGCA--AAGAATTCTAGTGGGAGAGATGCCATCTTCATCAAG 1242
 Db 1243 CTGACCAACTGAGTCAACCCAGCAGCTAGCTGAAGACGACACATGTTCTCTCAAG 1302
 QY 1243 GCCATTGTGGA 1253
 Db 1303 TGCATTGTGGA 1313

RESULT 10

US-10-085-117-329
 ; Sequence 329, Application US/10085117
 ; Publication No. US2003023234A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.
 ; APPLICANT: Engelhard, Eric K.
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 ; FILE REFERENCE: 52945200C121
 ; CURRENT APPLICATION NUMBER: US/10/085,117
 ; CURRENT FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: US 09/798,586
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 361
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 329
 ; LENGTH: 2380
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-085-117-329

Query Match 23.4%; Score 296.6; DB 15; Length 2380;
 Best Local Similarity 66.2%; Pred. No. 2.5e-76;
 Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

QY 586 CTGAGAGAAAGACGCCACTTTTGAGAACATTGTCTGCGTCTGAACCGGAGGTGGAG 645
 Db 643 CTGAGGGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 702
 QY 646 AGGTGGCCATGACTGCCGAGGCTTGAACCGGAGCAGCCGCTGGACCAAGACAGATT 705
 Db 703 GCCTCCACCTGGCCCTGGCCACTCTATCCACGAGCAGCTGGACCGTGAGCGCATC 762
 QY 706 GAAGCCCTGATGACAGGTGACAGCTGGAGAGGAGCATTTGGCCCTCAAGGACCTGGCG 765
 Db 763 CTGAGCTTGAGCAGAGGTGGTGGAGCTTCACAGACCTGGCCAGAAACACAGGCC 822
 QY 766 ATGGCTGACTTGAGCAGAGGTCTTTGGAGATGGAGGATCCACCTACGATGGGGTCTTC 825
 Db 823 CTGGCAAGCTGGAGCAGAGCTTGGCGCTCATGGAGAGGCTCTTCGATGGCACTTTC 882
 QY 826 ATCTGGAGATCTCAGACTTCGACGAGAGCTCCAGAGAGCTGTGGCTGGCCGATACCC 885
 Db 883 CTGTGGAAGATCAACCAATGTCACGAGCGGTGCGATGATGGCGCTGTGGCAGGACCGTC 942
 QY 886 GCATCTTCTCCCGAGCTTCTACACGAGGATGAGGTGAGGATGATGTTCTGGGTATC 945
 Db 943 AGCTCTTCTCCCGAGCTTCTACATGTCAGAGTATGGCTACAGTTGTGCTCGGCTG 1002
 QY 946 TACCTGAACGCGACGCGAGGAGGAGCAACACTGTGCTCTTCTTGTGTGTGATG 1005
 Db 1003 TACCTGAATGAGATGGCACTGGAAAGAGAACCCATCTGTGCTCTTCTATCGTGTATG 1062

RESULT 11

US-10-342-887-1184
 ; Sequence 1184, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 1184
 ; LENGTH: 2380
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-342-887-1184

Query Match 23.4%; Score 296.6; DB 16; Length 2380;
 Best Local Similarity 66.2%; Pred. No. 2.5e-76;
 Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

QY 586 CTGAGAGAAAGACGCCCACTTTTGAGAACATTGTCTGCGTCTGAACCGGAGGTGGAG 645
 Db 643 CTGAGGGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 702
 QY 646 AGGTGGCCATGACTGCCGAGGCTTGAACCGGAGCAGCCGCTGGACCAAGACAGATT 705
 Db 703 GCCTCCACCTGGCCCTGGCCACTCTATCCACGAGCAGCTGGACCGTGAGCGCATC 762
 QY 706 GAAGCCCTGATGACAGGTGACAGCTGGAGAGGAGCATTTGGCCCTCAAGGACCTGGCG 765
 Db 763 CTGAGCTTGAGCAGAGGTGGTGGAGCTTCAGCAGACCTGGCCAGAAACACAGGCC 822
 QY 766 ATGGCTGACTTGAGCAGAGGTCTTTGGAGATGGAGGATCCACCTACGATGGGGTCTTC 825
 Db 823 CTGGCAAGCTGGAGCAGAGCTTGGCGCTCATGGAGAGGCTCTTCTGATGGCACTTTC 882
 QY 826 ATCTGAAGATCTCAGACTTCGCGAGGAGATCCAGGAAGCTGTGGTGGCCGATACCC 885

Db 883 CTGTGGAAGATCAACCAATGTACACAGGCGGTGCCATGATGCGGCTGTGGCAGACCGTC 942
 QY 886 GCATCTTTCTCCCAAGCTTTCTACACAGCAGGTACGGCTACAAAGATGTGTGCGTATC 945
 Db 943 AGCCTCTTCTCCCAAGCTTTCTACACTGCCAAGTATGGCTACAAAGTTGTGCTGGGCTG 1002
 QY 946 TACCTGAACGGCGAGCGGACCGGCGAGGACACACCTGTCCCTCTTTTGTGCTGATG 1005
 Db 1003 TACCTGAATGGAGATGGCAGCTGGAAAGAACCATCTGTGCTCTTCATGCTGATCATG 1062
 QY 1006 AAGGCCCGAATAGCGCCCTCTGCGGTGGCCCTTCAACCAAGAGGTGACCTTAATGCTG 1065
 Db 1063 AGAGGGGAGTATGATGCGCTGCGGTGGCCCTTCCGAAACAGGTACCTTCATGCTG 1122
 QY 1066 CTCGACCAAGATACCGGAGCAGTGTGATTCAGCGCTTCAGGCGGCGAGCTGACTTCATCC 1125
 Db 1123 CTGGACCAAGAACACCGTGAGCAGCCATTGACGCTTTCGGGCTGACCTAAGCTCAGCG 1182
 QY 1126 TCTTTTCAGAGCCAGTCAACGACATGAACATCGAAGCGGCTGCCGCCCTCTTCTGCCCC 1185
 Db 1183 TCTTTCCAGAGGCCCGCAGAGTGAACCAACGCTGGCCAGTGGATGCCACCTCTTCTCCCC 1242
 QY 1186 GTCTCCAGATGGAGGCA---AAGAAATTCCTACGTGGGAGCATGCGATCTTCATCAAG 1242
 Db 1243 CTCAGCAACTGCACTACCCCAAGCAGCCTACGTGAAGGACGACACAATGTTCTCTCAAG 1302
 QY 1243 GCCATTGTGGA 1253
 Db 1303 TGCATTGTGGA 1313

RESULT 12
 US-10-044-090-823
 ; Sequence 823, Application US/10044090
 ; Publication No. US20020137081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olga Bandman
 ; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
 ; FILE REFERENCE: PA-0028 US
 ; CURRENT APPLICATION NUMBER: US/10/044,090
 ; CURRENT FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 850
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 823
 ; LENGTH: 5981
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020137081A1 228001.3
 US-10-044-090-823

Query Match 23.4%; Score 296.6; DB 13; Length 5981;
 Best Local Similarity 66.2%; Pred. No. 3.1e-76;
 Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;
 QY 586 CTGAGAGAGACGCGCCACTTTGAGACATTTCTGCGTCTTGAACCGGAGGTGGAG 645
 Db 1265 CTGAGGGGAAGCTGCGTGTGTTTGAACATTTGCTGCTCTCAACAAAGGAGGTGGAG 1324
 QY 646 AGGGTGGCCATGATCGCCAGCGCTGACGCGGAGCAGCGGCTGGACCAAGACAAGATT 705
 Db 1325 GCCTCCCACTGGCCCTGCGCCACCTCTATCCACAGAGCCAGCTGGACCGTGAGCGCATC 1384
 QY 706 GAAGCCCTGATAGCAAGGTGACGAGCTGAGAGAGCAATGGCCCTCAAGAGCCTGGCG 765
 Db 1385 CTGAGCTTGGAGCAGAGGGGTGGTGGAGCTTCAGCAGACCCCTGGCGCCCAAGAAAGCAGGCC 1444
 QY 766 ATGGCTGACTTGGAGCAGAAAGGTCTTGAGATGAGGAGCATCCACCTACGATGGGCTTTC 825
 Db 1445 CTGGCAAGCTGGAGCAGAGCTTGGCGCTCATGAGAGGCGCTCTTCGATGGCACTTTC 1504

QY 826 ATCTGGAATCTCAGACTTGGCCAGGAAGCTCCAGGAAGCTGTGGCTGGCGCATACCC 885
 Db 1505 CTGTGGAAGATCACCAATGTACACAGGCGGTGCCATGAGTGGGCTGTGGCAGGACCGTC 1564
 QY 886 GCATCTTTCTCCCAAGCTTTCTACACAGCAGGTACGGCTACAAAGATGTGTGCGTATC 945
 Db 1565 AGCCTCTTCTCCCAAGCTTTCTACACTGCCAAGTATGGCTACAAAGTTGTGCTGGGCTG 1624
 QY 946 TACCTGAACGGCGAGCGGACCGGCGAGGACACACCTGTCCCTCTTTTGTGCTGATG 1005
 Db 1625 TACCTGAATGGAGATGGCAGCTGGAAGAAACCCATCTGTGCTCTTTCATGCTGATCATG 1684
 QY 1006 AAGGCCCGAATAGCGCCCTCTGCGGTGGCCCTTCAACCAAGAGGTGACCTTAATGCTG 1065
 Db 1685 AGAGGGGAGTATGATGCGCTGCTGCGGTGGCCCTTCCGAAACAAAGGTACCTTCATGCTG 1744
 QY 1066 CTCGACCAAGATACCGGAGCAGCTGATTCAGCGCTTCAGGCGGCGAGCTGACTTCATCC 1125
 Db 1745 CTGGACCAAGAACACCGTGAGCAGCCATTGACGCTTTCGGGCTGACCTAAGCTCAGCG 1804
 QY 1126 TCTTTTCAGAGCCAGTCAACGACATGAACATCGAAGCGGCTGCCGCCCTCTTCTGCCCC 1185
 Db 1805 TCTTTCCAGAGGCCCGCAGAGTGAACCAACGCTGGCCAGTGGATGCCACCTCTTCTCCCC 1864
 QY 1186 GTCTCCAGATGGAGGCA---AAGAAATTCCTACGTGGGAGCATGCGATCTTCATCAAG 1242
 Db 1865 CTCAGCAACTGCACTACCCCAAGCAGCCTACGTGAAGGACGACACAATGTTCTCTCAAG 1924
 QY 1243 GCCATTGTGGA 1253
 Db 1925 TGCATTGTGGA 1935

RESULT 13
 US-10-453-478-7
 ; Sequence 7, Application US/10453478
 ; Publication No. US20030208043A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
 ; Jian Ni and Jing-Shan Hu
 ; TITLE OF INVENTION: Human Genes, Sequences and
 ; Expression Products
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CECCHIA, BYRNE, BAIN, GILFILLAN,
 ; CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/453,478
 ; FILING DATE: 04-Jun-2003
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/705,771
 ; FILING DATE: August 30, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MULLINS, J.G.
 ; REGISTRATION NUMBER: 33,073
 ; REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 973-994-1700
 ; TELEFAX: 973-994-1744
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2361 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-453-478-7

Query Match      21.8%; Score 276.8; DB 15; Length 2361;
Best Local Similarity 64.3%; Pred. No. 1.6e-70;
Matches 431; Conservative 0; Mismatches 237; Indels 2; Gaps 1;

QY 586 CTGGAGAGAAAGACGGCCACTTTGAGAACATTGTCTGCGTCTCTGAACCGGAGGTGGAG 645
Db      |||||
QY 645 CTGGAGGGGAAGCTGGTGTGTTGAGACATGTTGCTGTCTCTCAACAGAGGTGGAG 704
Db      |||||
QY 646 AGGGTGGCCATGACTCCGAGGCGCTGCAGCGGAGACACCGGTGGACCAAGACAAAGATT 705
Db      |||||
QY 705 GCCTCCCACTGGCCCTGGCCACTTATCCACAGAGCCAGCTGGACCGTGAGCGCATC 764
Db      |||||
QY 706 GAAGCCCTGAGTAGCAAGGTGCAGCAGCTGGAGAGGACATTGGCTCAAGGACCTGGCG 765
Db      |||||
QY 765 CTGAGCTTGGAGGAGGTTGTGCAAGTTCAAGACCTCTGAGACCCCTGCCAGAAACAGAGCC 824
Db      |||||
QY 766 ATGGCTGACTTGGAGCAGAAGTCTTTGGAGATGGAGGCATCCACCTACGATGGGTCTTC 825
Db      |||||
QY 825 CTGGGCAAGCTGGAGCAGAGCTTGGCCCTCATGGAGAGGCTCTCTTCGATGGCACTTC 884
Db      |||||
QY 826 ATCTGGAAGATCTCAGACTTCGCCAGAGCTCCAGGAGCTGTGGCTGGCCGATACCC 885
Db      |||||
QY 885 CTGTGGAAGATCAACAGTGTCAACAGGCGGTGCCATGAGTCGGCCCTGTGGCAGGACCGTC 944
Db      |||||
QY 886 GCATCTCTTCCCGAGCCCTTCTACACAGCAGGTACGGCTACAAGATGTCTGGGTATC 945
Db      |||||
QY 945 AGCTCTTCTCCCGAGCCCTTCTACACTGCCAAGTATGGCTACAAGTTGTGCTGGCGTG 1004
Db      |||||
QY 946 TACCTGAACGGCGACGGCAGCCGCGAGGAAACACACTGTCCCTCTCTTTTGTGTGATG 1005
Db      |||||
QY 1005 TACCTGATTGGAGATGGCATGCGTGAAGAAACCCATCTTTTCGCTCTTTCATCGTGATC 1064
Db      |||||
QY 1006 AAGGGCCCGAATGACGCCCTGTGCGGTGGCCCTTCAACAGAGTGACCTTAATGCTG 1065
Db      |||||
QY 1065 AGGGGGAGTATGATCGCTGTGCGGTGGCCCTTCCGGAACAGGTACCTTCATGCTG 1124
Db      |||||
QY 1066 CTCGACCAAGTAACCGGAGCAGCTGATGATGACGCTTCAGCCCGCAGCTGACTTCATCC 1125
Db      |||||
QY 1125 CTGGACCAAGAACACCGTGAGCAGCCATTGACGCTTCGGGCTGACCTTAAGCTCAGCG 1184
Db      |||||
QY 1126 TCTTTTCAGGCGCAGTCAACGACATGACATCGCAAGCGCTGCCCTCTCTTCTGCCCC 1185
Db      |||||
QY 1185 TCCTTCCAGAGGCCCCAGAGTGAAACCAACGTCGGCAGTGGATGGCCACTCTCTTCCCC 1244
Db      |||||
QY 1186 GTCTCCAAAGATGGAGCAAGAAATTCCTAC--GTGCGGAGCAGTGCATCTTTCATCAAGG 1243
Db      |||||
QY 1245 CTCAGCAAACTGCAGTCACCAAGCAGCGCTAGCTAAGGACGACACAAATGTTCTCAAGT 1304
Db      |||||
QY 1244 CATTGTGGA 1253
Db      |||||
QY 1305 GCATTGTGGA 1314
Db      |||||

RESULT 14
US-09-918-995-28886/c
; Sequence 28886, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
```

```

; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28886
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(481)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-28886

Query Match      21.4%; Score 272; DB 10; Length 481;
Best Local Similarity 100.0%; Pred. No. 2.6e-69;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 454 AAACAGCAGAGCAGCAGAGTGCAGTGTGCGGAGCACCTGCGCCATGTCTACTGAGTCG 513
Db      |||||
QY 480 AAACAGCAGAGCAGCAGAGTGCAGTGTGCGGAGCACCTGCGCCATGTCTACTGAGTCG 421
Db      |||||
QY 514 GTGCTGGAGCAAGCCCTCTTTGGGAGACCAAGCCAGCCGCGGGTCCAGAGCTCCGCGAG 573
Db      |||||
QY 420 GTGCTGGAGCAAGCCCTCTTTGGGAGACCAAGCCAGCCGCGGGTCCAGAGCTCCGCGAG 361
Db      |||||
QY 574 AGGTGCGAGAGCCCTGGAGAGAGACCGCCACTTTTTCAGAACATTTGTCGCTCCTGAAC 633
Db      |||||
QY 360 AGGTGCGAGAGCCCTGGAGAGAGAGAGCGCCACTTTTTCAGAACATTTGTCGCTCCTGAAC 301
Db      |||||
QY 534 CGGAGGTGGAGAGGTGGCGCATGACTGCGAGGCGCTGAGCCGCGGAGCAGCCGCGTGGAC 693
Db      |||||
QY 300 CGGAGGTGGAGAGGTGGCGCATGACTGCGAGGCGCTGAGCCGCGGAGCAGCCGCGTGGAC 241
Db      |||||
QY 694 CAACACAGATTGAAGCCCTGAGTAGCAAGT 725
Db      |||||
QY 240 CAACACAGATTGAAGCCCTGAGTAGCAAGT 209
Db      |||||

RESULT 15
US-10-085-117-327
; Sequence 327, Application US/10085117
; Publication No. US2003023234A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 52945200121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 327
; LENGTH: 1230
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-085-117-327

Query Match      21.4%; Score 272; DB 15; Length 1230;
Best Local Similarity 63.8%; Pred. No. 3.4e-69;
Matches 429; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 586 CTGGAGAGAGAGACGGCCACTTTTGAACATGTTGCGTCTCTGAACCGGAGGTGGAG 645
Db      |||||
QY 547 CTGGAGAGAGAGCTGCGTGTGTTTGAACATGTTGCTCTCTCAACAGGAGGTGGAG 606
Db      |||||
QY 646 AGGGTGGCCATGACTGCGGAGGCGCTGCAGCGGAGCAGCAGCCGCTGGACCAAGACAAAGATT 705
Db      |||||
QY 607 GCTTCCACACCTGGCACTGGCGGCTCCATCCACAGAGCCAGTTGGACCGGAGCACCTC 666
Db      |||||
QY 706 GAAGCCCTGAGTAGCAAGGTGACAGCTGAGAGAGGACATTTGCGCTCAAGAGCCTGGCG 765
Db      |||||
QY 667 CTGAGCTTGGAGCAGAGGTTGTGGAATTACAGAAACCCCTGGCTCAAAAGAGCAGGTC 726
Db      |||||
```

```
QY 766 ATGGCTGACTTGGAGCAGAGGTCTTGGAGATGAGGATCCACCTACGATGGGGTCTTC 825
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 727 CTGGCAGCTTGGACAGCTCTCGACTCATGGAGGAGCATCTTTGATGGTACTTTC 786
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 826 ATCTGGAAGATCTCAGACTTGGCAGGAAGCTCCAGGAAGCTGTGGCTGGCCGATACCC 885
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 787 CTGTGGAAGATCACCAGTGTCAACAAGCGGTGCCACGAGTCAGTGTGTGGCCGACTGTC 846
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 886 GCCATCTTCTCCCGAGCTTCTACACGACGAGTACGGCTACAGATGTGTCTGCGTATC 945
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 847 AGCCTCTTCTCTCAGCTTCTACCTGCCAAGTATGTTACAAGTTGTGCTGCGCTTG 906
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 946 TACCTGAACGGCGAGCGCACCGGGCGAGGAACACACCTGTCCCTCTTCTTTGGTGTATG 1005
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 907 TACCTGAACGGGGATGGCTCAGGCAAGAAAGACCCACCTGTCCCTCTTTCATCGTATCATG 966
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 1006 AAGGCCCGAATGACGCCCTCTGCTGGGTGGCCCTTCAACGAGAGTGAAGCTTAATGCTG 1065
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 967 AGAGGAGAAATACGATGCTCTCTGCCCCCTTTCAGGAACAAGGTACCTTTATGCTA 1026
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 1066 CTCGACCAAGATAACCGGGAGCAGTGTATTGACGCTTTCAGGCCCGCAGCTCACTTCATCC 1125
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 1027 CTTGACCAAGAACACCGAGAGCATGCTATTGATGCTTCCGGCTGACCTGAGCTCAGCC 1086
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 1126 TCTTTTCAGAGGCCAGTCAACGACATGAACATCGCAAGCGGCTGCCCCCTCTTCTGCCCCC 1185
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 1087 TCCTTCCAGCGGCCACAGAGTGAGACCAACGTTGGCCAGCGGCTGCCCGCTCTTCTTCCCC 1146
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 1186 GTCTCCAAAGATGGAGGCA--AAGAAATTCCTACGTGCGGACGATGCCATCTTCATCAAG 1242
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 1147 CTCAGCAAGCTGCAGTCAACCCAGCAGCCCTACGTCAAAGATGACACAATGTTCTCTCAA 1206
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 1243 GCCATTTGGGAC 1254
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
QY 1207 TGCATTGTGGAC 1218
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
```

Search completed: November 6, 2004, 23:46:30
Job time : 707 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 18:54:26 ; Search time 4401 Seconds
(without alignments)
10507.162 Million cell updates/sec

Title: US-10-018-030B-1

Perfect score: 1269

Sequence: 1 atggctgagctagctgac.....tggacctgacagggctctaa 1269

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1020.4	80.4	2193	3	CR611225	full-length
2	802	63.2	918	5	BU553823	AGENCOURT
3	771.6	60.8	857	4	EG677004	602623643
4	769	60.6	906	5	EX329304	EX329304
5	701	55.2	2993	3	AK052934	Mus muscu
6	699.4	55.1	2116	3	AK038136	AK038136
7	695	54.8	1506	9	AY413598	Homo sapi
8	647.8	51.0	668	6	CD630731	560712757
9	646.2	50.9	666	6	CD630730	560712758
10	631.4	49.8	934	5	BU857656	AGENCOURT
11	577.2	45.5	937	5	BU513753	AGENCOURT
12	573.2	45.2	578	4	BM790399	K-EST0070
13	498.6	39.3	1335	9	AY413599	Pan trogl
14	488	38.5	710	7	CK596664	AGENCOURT
15	486.2	38.3	495	2	AW882089	RC6-OT005
16	483.6	38.1	979	6	CB181509	AGENCOURT
17	453.4	35.7	881	5	EX370491	EX370491
18	447.6	35.3	551	2	BE683266	182742 MA
19	444.4	35.0	1506	9	AY413600	Mus muscu
20	439	34.6	835	7	CO566760	AGENCOURT
21	438.8	34.6	686	7	CK948654	4073760 B
22	437.4	34.5	1082	5	EX395088	EX395088
23	435.8	34.3	489	6	CB112836	K-EST0154
24	431.2	34.0	1073	1	AL526829	AL526829

25	427.8	33.7	855	7	CO574786	CO574786
26	427.2	33.7	585	7	CN432957	BEQ30005A
27	425.2	33.5	629	7	CO573496	AGENCOURT
28	422.4	33.3	603	1	AA619651	V101F10.1
29	412.4	32.5	442	4	EG392688	602410937
30	410.6	32.4	842	7	CF619315	AGENCOURT
31	404.2	31.9	433	4	BM797025	K-EST0079
32	403.4	31.8	511	5	BQ305193	MRO-BT200
33	399.2	31.5	640	7	CK944910	4069342 B
34	388.2	30.6	481	2	BF775206	285298 MA
35	388.2	30.6	513	5	BQ305196	MRO-BT200
36	388.2	30.6	941	1	AL547385	AL547385
37	373.6	29.4	976	5	EX398226	EX398226
38	372	29.3	477	2	BF775207	285299 MA
39	369	29.1	465	6	CB133303	K-EST0184
40	367.6	29.0	587	5	BP872066	BP872066
41	367.6	29.0	639	7	CN345159	170004705
42	367.6	29.0	729	4	EG385770	602454002
43	367.6	29.0	795	5	EX424592	EX424592
44	367.6	29.0	823	4	BI767443	603057596
45	367.6	29.0	879	4	BI093667	602859992

ALIGNMENTS

RESULT 1
LOCUS CR611225 2193 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODK009YH01 of HeLa cells Cot 25-normalized of Homo sapiens (human).
ACCESSION CR611225
VERSION CR611225.1 GI:50492032
KEYWORDS HTC; CNSUT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2193)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue
REFERENCE 2 (bases 1 to 2193)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
COMMENT - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
Location/Qualifiers
1..2193
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK009YH01"
/tissue type="HeLa cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"

Query Match 80.4%; Score 1020.4; DB 3; Length 2193;
Best Local Similarity 84.2%; Pred. No. 1.2e-235;
Matches 1268; Conservative 0; Mismatches 1; Indels 237; Gaps 1;
QY 1 ATGGCTGAGCTAGCTGACGCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC 60
DB 24 ATGGCTGAGCTAGCTGACGCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC 83


```

ORIGIN
Query Match 63.2%; Score 802; DB 5; Length 918;
Best Local Similarity 97.7%; Pred. No. 6.7e-183;
Matches 856; Conservative 0; Mismatches 15; Indels 4; Gaps 4;

QY 395 AGTGTGAGTCCCTTGCAGATTCACGCCATCGCTGCTCGAGACGGTAGAGGTGAGA 454
DB 1 AGTGTGAGTCCCTTGCAGATTCACGCCATCGCTGCTCGAGACGGTAGAGGTGAGA 60
QY 455 AACACGAGGACGACGAGGTGAGTGGCTGCGGGAGCACCTTGGCCATGCTACTGAGCTGG 514
DB 61 AACACGAGGACGACGAGGTGAGTGGCTGCGGGAGCACCTTGGCCATGCTACTGAGCTGG 120
QY 515 TGCTGAGGCAAGCCCTTCTGGAGACGAGACGCGGGGTTCAGAGTCTCTGCGAGA 574
DB 121 TGCTGAGGCAAGCCCTTCTGGAGACGAGACGCGGGGTTCAGAGTCTCTGCGAGA 180
QY 575 GGTGCGAGGCTGCGAGAGGAGAGGACGCGCACCTTTTGAGAACATTTCTGCGCTCTGGAAC 634
DB 181 GGTGCGAGGCTGCGAGAGGAGAGGACGCGCACCTTTTGAGAACATTTCTGCGCTCTGGAAC 240
QY 635 GGGAGGTGAGAGGTGGCGATGATGCGCGAGGCTGCGAGCGGAGGACGCGGTGGAC 694
DB 241 GGGAGGTGAGAGGTGGCGATGATGCGCGAGGCTGCGAGCGGAGGACGCGGTGGAC 300
QY 695 AAGACAGATTCAAGCCCTGAGTACAGAGTGCAGAGTGCAGAGGAGGATTTGGCTCA 754
DB 301 AAGACAGATTCAAGCCCTGAGTACAGAGTGCAGAGTGCAGAGGAGGATTTGGCTCA 360
QY 755 AGGACCTGCGGATGCTGATCTTGGAGCAAGAGTCTTGGAGATGAGGACATCCACTAG 814
DB 361 AGGACCTGCGGATGCTGATCTTGGAGCAAGAGTCTTGGAGATGAGGACATCCACTAG 420
QY 815 ATGGGGTCTTCATCTGGAAGATCTCAGACTTCGCGAGGAGCTCCAGGAGGTGGCTG 874
DB 421 ATGGGGTCTTCATCTGGAAGATCTCAGACTTCGCGAGGAGCTCCAGGAGGTGGCTG 480
QY 875 GCGCATACCGGCACTTTCTCCAGCCTTCTACACGAGGATGAGGCTACAGAGTGT 934
DB 481 GCGCATACCGGCACTTTCTCCAGCCTTCTACACGAGGATGAGGCTACAGAGTGT 540
QY 935 GTCTGGGTATCTACCTGAACGCGGACGCGACCGGGGAGGAAACACCTGCTCTTCT 994
DB 541 GTCTGGGTATCTACCTGAACGCGGACGCGACCGGGGAGGAAACACCTGCTCTTCT 600
QY 995 TTGTGGTGTAGAGGCGCGATGAGCGCTCTGCGTGGCGCTTCAACCAAGAGTGA 1054
DB 601 TTGTGGTGTAGAGGCGCGATGAGCGCTCTGCGTGGCGCTTCAACCAAGAGTGA 660
QY 1055 CCTTAATGCTGCTCGACCAAGATTAACCGGGAGCAGTGATTCAGCGCTTACGGCCGACG 1114
DB 661 CCTTAATGCTGCTCGACCAAGATTAACCGGGAGCAGTGATTCAGCGCTTACGGCCGACG 720
QY 1115 TGACTTCACTCTTTTCAGAGCGGATCAAGGACATGAACATGCGACGCGG--CTGCCC 1172
DB 721 TGACTTCACTCTTTTCAGAGCGGATCAAGGACATGAACATGCGACGCGGCTGCCCC 780
QY 1173 CTTCTTCTGCCCCGCTTCAAGAT--GGAGGCAAGAAATTCCTACGT--GCGGACAGTGC 1230
DB 781 CTTCTTCTGCCCCGCTTCAAGATGAGGCGCAAGAAATTCCTACGTGCGGCGACGATGC 840
QY 1231 ATCTTCATC--AAGGCAATGTGACCTGACAGGCT 1265
DB 841 TTCTTCAATCAAGGCAATTTGGACCTGACAGGCT 876

RESULT 3
BG677004 857 bp mRNA linear EST 01-MAY-2001
LOCUS 602623643F1 NCI_CGAP_skn4 Homo sapiens cDNA clone IMAGE:4748555 5',
DEFINITION mRNA sequence.
ACCESSION BG677004

```

```

BG677004.1 GI:13908401
EST. Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 857)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10600 row: f column: 12
High quality sequence stop: 847.
FEATURES
Location/Qualifiers
1..857
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4748555"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP Skn4"
/notes="Organ: Skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 60.8%; Score 771.6; DB 4; Length 857;
Best Local Similarity 98.3%; Pred. No. 1.5e-175;
Matches 843; Conservative 0; Mismatches 9; Indels 6; Gaps 6;

QY 400 CGAGTCCCTTGCAGATTCACGCCATCGCTGCTCGAGACGGTAGAGGTGAGAACAG 459
DB 1 CGAGTCCCTTGCAGATTCACGCCATCGCTGCTCGAGACGGTAGAGGTGAGAACAG 60
QY 460 CAGAGACACAGAGTGCA- GTGGCTGCGGAGACACCTGGCCATGCTACTGAGCTCGGTGCT 518
DB 61 CAGAGACACAGAGTGCA GTGGCTGCGGAGACACCTGGCCATGCTACTGAGCTCGGTGCT 120
QY 519 GGAGGCAAGCCCTCTTGGAGACAGAGCCAC- GCGGGGTGAGAGCTCTCTGCAAGGT 577
DB 121 GGAGGCAAGCCCTCTTGGAGACAGAGCCAC- GCGGGGTGAGAGCTCTCTGCAAGGT 180
QY 578 GCGAGAGCTTGGAGAGAGACCGCCACTTTTGAGAACATTTGCTGCTGCTGAAACCGGG 637
DB 181 GCGAGAGCTTGGAGAGAGACCGCCACTTTTGAGAACATTTGCTGCTGCTGAAACCGGG 240
QY 638 AGGTGGAGAGGTGGCCATGACTGCCAGGCTGCGAGCGGACGCGGCTGGACCAAG 697
DB 241 AGGTGGAGAGGTGGCCATGACTGCCAGGCTGCGAGCGGCTGCGAGCGGCTGGACCAAG 300
QY 698 ACAAGATTGAAGCCCTGAGTAGCAAGGTGAGAGCTGGAGAGAGCAATTTGGCTCAAGG 757
DB 301 ACAAGATTGAAGCCCTGAGTAGCAAGGTGAGAGCTGGAGAGAGCAATTTGGCTCAAGG 360
QY 758 ACCTGGCGATGGCTGACTTGGAGAGAGGTCTTGGAGATGGAGGATCCACCTACCATG 817
DB 361 ACCTGGCGATGGCTGACTTGGAGAGAGGTCTTGGAGATGGAGGATCCACCTACCATG 420
QY 818 GGGTCTTCATCTGGAAGATCTCAGACTTCGCGAGGAGCTCCAGGAAAGCTGTGGCTGGCC 877
DB 421 GGGTCTTCATCTGGAAGATCTCAGACTTCGCGAGGAGCTCCAGGAAAGCTGTGGCTGGCC 480
QY 878 GCATACCGCGCATCTTCTCCGCCACCTTCTACACAGAGGTA CGGCTACAAGATGTGTC 937

```


Db 481 GAATACCCGCCATCTTCTCCACAGCTTCTACACAGAGGTACGGCTACAGATGTCTC 540
 QY 938 TCGGTATCTACTGAAACGGCGAGCAGCCGGCGAGGAGAACACACCTGCTCTCTTTTG 997
 Db 541 TCGGTATCTACTGAAACGGCGAGCAGCCGGCGAGGAGAACACACCTGCTCTCTTTTG 600
 QY 998 TGGTATGAAGGCGCCGAAATACGCCCTGCTGCGGTGCGCCCTTCAACAGAGGTGACCT 1057
 Db 601 TGGTATGAAGGCGCCGAAATACGCCCTGCTGCGGTGCGCCCTTCAACAGAGGTGACCT 660
 QY 1058 TAATGCTGCTCGACAGAAATAACCGGAGCAGCTGATTGACGCCCTTCAGGCGCCGACGTGA 1117
 Db 661 TAATGCTGCTCGACAGAAATAACCGGAGCAGCTGATTGACGCCCTTCAGGCGCTGACGTGA 720
 QY 1118 CTTCATCTCTTTTTCAGAGGCCAGTCACAGACA-TGAACATCGCAAGGGGTGCGCCCTC 1176
 Db 721 CTTCATCTCTTTTTCAGAGGCCAGTCACAGACA-TGAACATCGCAAGGGGTGCGCCCTC 780
 QY 1177 TTCTGCCCC-GTCTCCAGA-TGGAGGCAAAAGAAATTCCTAGTGGGAGCAGATGCCATCT 1234
 Db 781 TTCTGCCCCGTCTCCAGATTTGGAGGCAAGAAATTCCTAGTGGGAGCAGATG-CACT 839
 QY 1235 TCATCAAGGCCATTTGTG 1252
 Db 840 TCATCAAGGCCATTTGTG 857

RESULT 4
 LOCUS BX329304/c
 DEFINITION BX329304 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 cDNA clone CS0DK009YH01 3-PRIME, mRNA sequence.
 VERSION BX329304
 KEYWORDS BX329304.1 GI:30346570
 SOURCE EST.
 ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1. (Bases 1 to 906)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 5308.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?sa=CS0BA1039ZH08_CS03712_1&c=5308.f

FEATURES
 source Location/Qualifiers
 1..906
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DK009YH01"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /call_line="HELA"
 /clone_lib="HELA"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized."

ORIGIN

Query Match 60.6%; Score 769; DB 5; Length 906;

Best Local Similarity 97.8%; Pred. No. 6.3e-175;
 Matches 831; Conservative 0; Mismatches 13; Indels 6; Gaps 5;
 QY 420 CGCCATCGGCTGCTCGAGACGGTACAGGTTAGAAACAGCAGGAGCAGAGTGCAGTG 479
 Db 906 CGCCATCGGCTGCTCGAGACGGTACAGGTTAGAAACAGCAGGAGCAGAGTGCAGTG 847
 QY 480 GCTGCGGAGCACTGCGCCATCTACTAGCTCGGTGCTGAGGCAAAAGCCCTCTTGGG 539
 Db 846 GCTGCGGAGCACTGCGCCATCTACTAGCTCGGTGCTGAGGCAAAAG-CCTCTCTGGG 788
 QY 540 AGACACAGACCCACGCGGGGTACAGAGCTCTGTCAGAGGTGCGAGAGCCTTGGAGCAAGAC 599
 Db 787 AGACACAGACCCACGCGGGGTACAGAGCTCTGTCAGA-GTGGAGAGCCT-GAGAAAGAC 730
 QY 600 GGCACATTTTGTAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 659
 Db 729 GGCACATTTTGTAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 671
 QY 660 TGCAGAGGCTGCGAGCCGCGCAGCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 719
 Db 670 TGCAGAGGCTGCGAGCCGCGCAGCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611
 QY 720 CAAGGTGACAGCTGCGAGAGGAGCAATTTGGCTCAAGGACCTGGCGATGGCTGCTGCTG 779
 Db 610 CAAGGTGACAGCTGCGAGAGGAGCAATTTGGCTCAAGGACCTGGCGATGGCTGCTGCTG 551
 QY 780 GCAGAGGTCTTTGGAGATGGAGGATCCACCTACGATGGGTCTTCATCTGGAAGATCTC 839
 Db 550 GCAGAGGTCTTTGGAGATGGAGGATCCACCTACGATGGGTCTTCATCTGGAAGATCTC 491
 QY 840 AGACTTTCGCCAGGAGAGCTTCCAGGAGAGCTGTGGCTGGCGCAGATCCCGCATCTTCTC 899
 Db 490 AGACTTTCGCCAGGAGAGCTTCCAGGAGAGCTGTGGCTGGCGCAGATCCCGCATCTTCTC 431
 QY 900 AGCTTCTACACAGCAGGTAGCGGTACAAAGATGTGTCTGCTGCTGCTGCTGCTGCTGCTG 959
 Db 430 AGCTTCTACACAGCAGGTAGCGGTACAAAGATGTGTCTGCTGCTGCTGCTGCTGCTGCTG 371
 QY 960 CGGACCCGGCGGAGGAGAACACACCTGCTCTCTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1019
 Db 370 CGGACCCGGCGGAGGAGAACACACCTGCTCTCTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 311
 QY 1020 GGCCTGCTGCGGTGGCCCTTCAACAGAGAGGTGACCTTAATGTGTGTGTGTGTGTGTGTGT 1079
 Db 310 GGCCTGCTGCGGTGGCCCTTCAACAGAGAGGTGACCTTAATGTGTGTGTGTGTGTGTGTGT 251
 QY 1080 CCGGAGCAGCTGATTGACGCTTTCAGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1139
 Db 250 CCGGAGCAGCTGATTGACGCTTTCAGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
 QY 1140 AGTCAACGACATGAACATCGCAAGCGGTGCGCCCTCTTCTGCCCCCTCTCCAGATGGA 1199
 Db 190 AGTCAACGACATGAACATCGCAAGCGGTGCGCCCTCTTCTGCCCCCTCTCCAGATGGA 131
 QY 1200 GCGAAGAAATTCCTACGTCGGGAGCATGCCATTTTCATCAAGGCCATTTGTGACCTGAC 1259
 Db 130 GCGAAGAAATTCCTACGTCGGGAGCATGCCATTTTCATCAAGGCCATTTGTGACCTGAC 73
 QY 1260 AGGGCTCTAA 1269
 Db 72 AGGGCTCTAA 63

RESULT 5
 AK052934
 LOCUS AK052934
 DEFINITION Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
 library, clone: D830048A10 product: rnf receptor-associated factor 2,
 full insert sequence.
 ACCESSION AK052934
 VERSION AK052934.1 GI:26343104
 KEYWORDS HTC; CAP trapper.

SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	Carninci, P. and Hayashizaki, Y.	
TITLE	High-efficiency full-length cDNA cloning	
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE	99279253	
PUBMED	10349636	
REFERENCE		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	
MEDLINE	20499374	
PUBMED	11042159	
REFERENCE		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)	
MEDLINE	20530913	
PUBMED	11076861	
REFERENCE		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.	
TITLE	Functional annotation of a full-length mouse cDNA collection	
JOURNAL	Nature 409, 685-690 (2001)	
MEDLINE		
PUBMED		
REFERENCE		
AUTHORS	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
JOURNAL	Nature 420, 563-573 (2002)	
MEDLINE		
PUBMED		
REFERENCE		
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://phantom.gsc.riken.jp/ Location/Qualifiers 1. .2993	
FEATURES	source	

/organism="Mus musculus"	
/mol_type="mRNA"	
/strain="C57BL/6J"	
/db_xref="FANTOM_DB:D830048A10"	
/db_xref="taxon:10090"	
/clone="D830048A10"	
/tissue_type="heart"	
/clone_lib="RIKEN full-length enriched mouse cDNA library"	
/dev_stage="16 days neonate"	
60..1565	
/notes="unnamed protein product; Tnf receptor-associated factor 2 (MGD) [MGI:101835, GB L35303, evidence: BLASTN, 99%, match=2097]"	
putative"	
/codon_start=1	
/protein_id="BAC35209.1"	
/db_xref="GI:26343105"	
/translation="MAAASVSPGSLLELPQSPKLLTGLRLKALYKLSACKNLRPP FQAQCHRYVCSFLTSILSGPQNCACVVEGLYEEGILSESSSAPFNAARREVS LPVPCNDGCTGKGLTKEYESGHEGCPFLLTETPCACKGLRLSEKHEHTEBCPCRS LSCQHCRAPCSHVDLEHVVECPFLTYDGGCKKIPRETFOHVRACSKRVLQRF HTVQCSREMYETENLODHELRHLALLSSFLQAQSPGTNLQVGPGLLOQCILE OKIATFENIVCVLNREVERVAVTAECSSQRLDQDKIEALSNNKVOQLERSIGLKDLA MADLEBKVSELEVSTVDGVFIWKISDFTRKQAEAVAGRTPALPSPAFYISRYGKNCL RYVLNGDVGTRGTHLSLFFVVMGPNDAILLQWPFNOKVITMLLDHNNRHRVIDAFRPD VTSSSFQRPVSDMNIAISGCPFLFCFVSKMEAKNSYVRDDAIFIKAIIVDLTGL"	
ORIGIN	
Query Match 55.2%; Score 701; DB 3; Length 2993;	
Best Local Similarity 71.0%; Pred. No. 2.2e-158;	
Matches 106; Conservative 0; Mismatches 200; Indels 237; Gaps 1;	
Qy 1 ATGCTCAGCTAGCGTGACCCCGCTGGCTCCTCGAGTTGTACAGCCGCTTCTCC 60	
Db 60 ATGCTCAGCGCAGTGTGACTTCCCTGGCTCCTAGAACTGTACAGCGCTGCTCC 119	
Qy 61 AAGACCTCTCTGGGACCAAGCTGGAGCCAACTGCTGCTCCCTCCAGAAAGTC 120	
Db 120 AAGACCTCTCTGGGACCAAGCTGGAGCCAACTGCTGCTCCCTCCAAAGATC 179	
Qy 121 CTCGCGAGGCGCTTCCAGGCGCAGTGTGGCCACCGTACTGCTCTTCTGCTGGCAGC 180	
Db 180 CTGCGAGGCGCTTCCAGGCGCAGTGTGGCCACCGTACTGCTCTTCTGCTGACCGC 239	
Qy 181 ATCTCAGCTCTGGGCTCAGAACTGCTGCTCCTCGAGTTGTACAGGCGCATATGAGAA 240	
Db 240 ATCTCAGCTCTGGGCGCCAGAACTGCTGCTCCTCGAGTTGTATGAGGCGCTGTATGAGAA 299	
Qy 241 GGCAATTTCTATTTTAGAAACAGTTGGCGCTTCCAGATAATGCTGCCCGCAGGAGGTG 300	
Db 300 GGCATTTCTATTTTAGAGAGTAGTTGGCCCTTTCCAGATACCGTCCCGCAGAGAGGTG 359	
Qy 301 GAGAGCTGCGGCGCGTCTTCCAGTGTATGATGACCTGGAAGGGGACCTCGAAAGAA 360	
Db 360 GAGAGCTGCGGCGCGTCTTCCAGTGTATGATGACCTTGAAGGGGACCTTGAAGAA 419	
Qy 361 TAGCA----- 365	
Db 420 TAGAGAGCTGCCACGAAAGACTTTGCCCAATTCTGCTGAGGAGGTGCTCTGATGATAA 479	
Qy 366 ----- 365	
Db 480 GGCCTGCTCGCGCTCAGCGAGAGGAGCACCACACTGAGCAGGAATGCCCCCAAGAGC 539	
Qy 366 ----- 365	
Db 540 CTGAGCTGCCAGCAGCTGACAGGACCGCTGTAGCCACGTGGACCTGGAGGTACTACTATGAG 599	
Qy 366 ----- 365	
Db 600 GTCTGCCCCAAGTTTCCCTTAACTATGCTGTGGCAAGTGTGGAGTCCCTCGGAG 659	
Qy 366 --GTTTCAGGACCAAGCTCAAGACTTGTGGCAAGTGTGGAGTCCCTTCAGATTCCACGCC 423	

[illegible]

```
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM DB:Al30081B14"
/db_xref="taxon:10090"
/clone="Al30081B14"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stages="16 days neonate"
60_1565
CDS
/notes="unnamed protein product; Tnf receptor-associated
factor 2 (MD) [MG1:101835, GB|L35303, evidence: BLASTN,
99%, match=2097]
putative"
/codon_start=1
/protein_id="BAC29937.1"
/db_xref="GI:26332439"
/translation="MAASVTSPPGSLLELLQPFQSTLLGTRLEAKYLCSACKNLRPP
FOQGHRYCSFCLTSIUSGPNCAACVYIEEGISILESSAFDPAARREVS
LPAVCPNCTWKGLKEYESCHEPLFLTECPACKGLVRLSEKHEHTBOEPKRS
LSCCHRAPCSHVDLEHYEVCPEPLTCDGCKKI PRETFQDHRVACSKVLCRF
HTVCGSEVETENLOHLELRLLEALLLSFLEAQAQSGTLNQVGPQLLQRCIILE
OKIATFENVCLVNSREVERVAVTAEACSRHRLDQKIEALSNKVOQLERSIGKDLA
MADLQKVSLESYDGVFIWKISDFTKEQCEAVAGTPALFSPAFVTSVGYKML
RYLNGDGTGRGTHLSLFVVMKGNDAALLQWPNQKVTMLLDHNNREHVIDAFRPD
VTSSSFQRPVSDMNIASGCLPFCPPVKMEAKNSYVRDDAIFIKAIVDLTGL"
2092..2097
polyA_signal
/notes="putative"
2116
polyA_site
/notes="putative"
```

ORIGIN

```
Query Match      55.1%; Score 699.4; DB 3; Length 2116;
Best Local Similarity 70.9%; Pred. No. 5e-158;
Matches 1067; Conservative 0; Mismatches 201; Indels 237; Gaps 1;

  1  ATGGCTGACGTAGCTGACCCCTGCTGCTCCCTGGAGTGTCTACAGCCCGCTTCTCC 60
  60  ATGGCTGACGACGAGTGTGATCTTCCCTGGCTCCCTAGAACTGCTACAGCTGGCTTCTCC 119
  120  CAGACCTCTCTGGGACCAAGGTAGAACCAAGTACCTCTGTTCAGCTTGCACCAATC 179
  181  AAGACCTCTCTGGGACCAAGGTAGAACCAAGTACCTCTGTTCAGCTTGCACCAATC 240
  240  ATCTCTCAGCTTGGGACCAAGGTAGAACCAAGTACCTCTGTTCAGCTTGCACCAATC 299
  241  GGCAATTTCTATTTAGAAAGCAGTTCGGCTTCCAGATAAATGCTGCCCGCAGGAGGTG 300
  300  GGCAATTTCTATTTAGAGAGTATTCGGCTTTCAGATAAAGCTGCCCGCAGAGAGGTG 359
  301  GAGAGCTTCCGCGCTCTGCTCCAGTATGATGACCTTGAAGGGGACCTTGAAGAA 360
  360  GAGAGCTTCCGCGCTCTGCTCCAGTATGATGACCTTGAAGGGGACCTTGAAGAA 419
  361  TACGA----- 365
  420  TACGAGAGCTGCCACGAAGGACTTTGCCCATCTCTGCTGACGGAGTCTCTGCTGATGAA 479
  366  ----- 365
  480  GGCCTGTGCTCCGCTCAGCGAGAGAGGAGCACCACTGAGCAGGAATGCCCAAGGAGC 539
  366  ----- 365
  540  CTGAGCTGCCGACTGACAGACACCTCTGAGCCAGTGGACCTGGAGGTACACTATGAG 599
  366  ----- 365
```

RESULT 7
AY413598
LOCUS

AY413598 1506 bp DNA linear GSS 17-DEC-2003
Homo sapiens TRAF2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

```
Db 600 GTCTGCCCAAGTTTCCCTTAACCTGTGATGGCTGTGCAAGAAGAGATCCCTCGGGAG 659
QY 366 --GTTTCAGGACCAAGTCAAGACTTGTGCAAGTGTGCAAGTCCCTTGCAGATTCCAGGCC 423
Db 660 ACGTTTCAGGACCAAGTGTGATGAGCATGAGCAATGCGGGTCTCTGCGAGATTCCACACC 719
QY 424 ATCGGTGCTCTCAGACGCTGAGAGGTGAGAAACAGACGAGACGACGAGTGCAGTGGCTG 483
Db 720 GTTGGCTGTTTTCAGAGATGTTGAGAGATGAGAACTGCAAGATCATGAGTGTGACGCGCTA 779
QY 484 CCGGAGCACCTGCGGCTTGTCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTG 543
Db 780 CCGGAGCACCTGAGCTTGTCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTG 839
QY 544 CAGAGCCACGCGGGGTGAGAGTCTCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 603
Db 840 TTGAACCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 899
QY 604 ACTTTTCAGAACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
Db 900 ACCTTTCAGAACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 959
QY 664 GAGGCTGACGCGGGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 723
Db 960 GAGGCTGACGCGGGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1019
QY 724 GTGACGAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 783
Db 1020 GTGCAACAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1079
QY 784 AAGGCTTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 843
Db 1080 AAGGCTTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1139
QY 844 TTCGCCAGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 903
Db 1140 TTCACCAAGAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1199
QY 904 TTCTACACCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 963
Db 1200 TTCTACACCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1259
QY 964 ACCGGGCGAGGAAACACACCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1023
Db 1260 ACTGGGCGGGAACATCATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1319
QY 1024 CTGCTGCGGTGGGCTTCAACCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1083
Db 1320 CTGTTGCAAGTGGGCTTCAACCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1379
QY 1084 GAGCAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1143
Db 1380 GAGCAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1439
QY 1144 AACGACATGAACATCGCAAGCGGTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1203
Db 1440 AGTGACATGAACATCGCAAGCGGTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1499
QY 1204 AAGATTTCTACGTCGCGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1263
Db 1500 AAGATTTCTACGTCGCGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1559
QY 1264 CTCTA 1268
Db 1560 CTCTA 1564
```

ACCESSION AY413598
 VERSION AY413598.1 GI:39769560
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 1506)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1506)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (18-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment...
 FEATURES
 source Location/Qualifiers
 1..1506
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>1506
 /gene="TRAP2"
 /locus_tag="HCM4944"
 ORIGIN
 Query Match 54.8%; Score 695; DB 9; Length 1506;
 Best Local Similarity 52.5%; Pred. No. 5.4e-157;
 Matches 942; Conservative 0; Mismatches 327; Indels 237; Gaps 1;
 QY 1 ATGGCTGAGCTAGCTGACCCCTCCCTGGCTGCTGAGTGTCTACAGCCCGCTCTCC 60
 DB 1 ATGGCTGAGCTAGCTGAGCCCTCCCTGGCTGCTGAGTGTCTACAGCCCGCTCTCC 60
 QY 61 AAGACCTCTCTGGGACCAAGCTGGAACCAAGTACCTGTCTCCGCTCGAGAAACGTC 120
 DB 61 AAGACCTCTCTGGGACCAAGCTGGAACCAAGTACCTGTCTCCGCTCGAGAAACGTC 120
 QY 121 CTCGCGAGCCCTTCCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTGCTGGCCAGC 180
 DB 121 CTCGCGAGCCCTTCCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTGCTGGCCAGC 180
 QY 181 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGTTTCCAGGGCATATATGAAGAA 240
 DB 181 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGTTTCCAGGGCATATATGAAGAA 240
 QY 241 GGCATTTCTATTAGAAAGCAGTTCGGCTTCCCGATTAATCTGCTCCGCGAGGAGTG 300
 DB 241 GGCATTTCTATTAGAAAGCAGTTCGGCTTCCCGATTAATCTGCTCCGCGAGGAGTG 300
 QY 301 GAGAGCTGCGGCGCTCTGCTCCAGTGTGATGACCTGGAAGGGGACCTGGAAGAA 360
 DB 301 GAGAGCTGCGGCGCTCTGCTCCAGTGTGATGACCTGGAAGGGGACCTGGAAGAA 360
 QY 361 TAGC----- 364
 DB 361 TAGCAGAGCTGCCACGAAGCCGCTGCCGCTCATGCTGACCGAATGCTCCGCGTCAAA 420
 QY 365 ----- 364
 DB 421 GGCTGTCCGCTTGTGTAAGAGGAGCGCCACCTGGAGCAGAGTGGCGGAGAGAC 480
 QY 365 ----- 364

RESULT 8

DB 481 CTGAGCTGCCGCAATGCGGGCACCCCTGCTGGAGCAGACGTGAAGGCGCACCCAG 540
 QY 365 ----- 364
 DB 541 GTCTGCCCAAGTTCCCTTAACCTTGTCGGCTGGGCAAGAAAGATCCCCGGGAG 600
 QY 365 -AGTTTCAGACCAAGCTCAAGCTTGTGCAAGTGTGAGTCCCTTGCAGATTCACGCC 423
 DB 601 AAGTTTCAGACCAAGCTCAAGCTTGTGCAAGTGTGAGTCCCTTGCAGATTCACGCC 660
 QY 424 ATCGGCTGCTCGAGACGCTAGAGGCTGAGAAACAGCAGGACGAGGTGAGTGGTG 483
 DB 661 ATCGGCTGCTCGAGACGCTAGAGGCTGAGAAACAGCAGGACGAGGTGAGTGGTG 720
 QY 484 CGGAGCACCTGGCCATGCTACTGAGCTCGGTGCTGGAGGCAAGCCCTCTTTGGGAG 543
 DB 721 CGGAGCACCTGGCCATGCTACTGAGCTCGGTGCTGGAGGCAAGCCCTCTTTGGGAG 780
 QY 544 CAGAGCCAGCGGGCTCAGAGCTCTCTGAGAGTGTGAGAGGCTGGAGAGGAGAGCGCC 603
 DB 781 CAGAGCCAGCGGGCTCAGAGCTCTCTGAGAGTGTGAGAGGCTGGAGAGGAGAGCGCC 840
 QY 604 ACTTTTGAAACATTTGCTGCTGCTGAAACCGGAGGTGGAGAGGTGGCCATGCTGCC 663
 DB 841 ACTTTTGAAACATTTGCTGCTGCTGAAACCGGAGGTGGAGAGGTGGCCATGCTGCC 900
 QY 664 GAGGCTGCTGAGCCGCGAGCAGCCGCTGGACCAAGATTGAAGCCCTGAGTAGCAAG 723
 DB 901 GAGGCTGCTGAGCCGCGAGCAGCCGCTGGACCAAGATTGAAGCCCTGAGTAGCAAG 960
 QY 724 GTGCAGCAGCTGGAGAGGACATTTGGCTCAAGGACCTGGCGATGCTGAGGAG 783
 DB 961 NNN 1020
 QY 784 AAGGCTTTGGAGATGGAGGCATCCACCTACGATGGGGTCTTTCATCTGGAAGATCTCAGAC 843
 DB 1021 NNN 1080
 QY 844 TTCGCCAGGAGCTCCAGGAGCTGTGGCTGGCGCATACCGGCACTTCTCCCGAGCC 903
 DB 1081 NNN 1140
 QY 904 TTCTACACAGCAGGTACGGCTACAAGATGTGTCTGCTATCTTACCTGAAACGGC 963
 DB 1141 NNN 1200
 QY 964 ACCGGCGAGGAAACACACCTGTCCTCTTCTTGTGTGATGAAGGGCCGAAATGACGCC 1023
 DB 1201 NNN 1260
 QY 1024 CTGCTGCGGTGCCCTTCAACAGAGAGGTGACCTTAATGTGCTCGACCAAGAAACCGG 1083
 DB 1261 NNN 1320
 QY 1084 GAGCAGTGTGAGCGCTTCAAGCCCGAGTGTGATCTTCTTTCAGAGCCGAGTC 1143
 DB 1321 GAGCAGTGTGAGCGCTTCAAGCCCGAGTGTGATCTTCTTTCAGAGCCGAGTC 1380
 QY 1144 AACGACATGAACATCGAAGCGGTGCCCTCTTCTGCGCGCTCCAGATGGAGGCA 1203
 DB 1381 AACGACATGAACATCGAAGCGGTGCCCTCTTCTGCGCGCTCCAGATGGAGGCA 1440
 QY 1204 AAGAAATCTTACGTGCGGAGCGATGCCATTTTCAAGGCCATTTGTGACCTGACAGG 1263
 DB 1441 AAGAAATCTTACGTGCGGAGCGATGCCATTTTCAAGGCCATTTGTGACCTGACAGG 1500
 QY 1264 CTCTAA 1269
 DB 1501 CTCTAA 1506

CD630731 56071275J1 FLP Homo sapiens cDNA, mRNA linear EST 12-JAN-2004
LOCUS 669 bp mRNA linear EST 12-JAN-2004
DEFINITION 56071275J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630731
VERSION CD630731.1 GI:40278997
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 669)
AUTHORS Fu, G.X., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com
FEATURES
source
1..669
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
ORIGIN
Query Match 51.0%; Score 647.8; DB 6; Length 668;
Best Local Similarity 99.7%; Pred. No. 1.2e-145;
Matches 649; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 405 CCCTTCAGATTCCAGCCATCGGCTCGCTCGAGACGGTAGAGGTGAGAAACAGCAGGA 464
DB 1 CCCTTCAGATTCCAGCCATCGGCTCGCTCGAGACGGTAGAGGTGAGAAACAGCAGGA 60
QY 465 GCACGAGGTGACGTGGCTGGGAGACACCTGGCCATGCTACTGAGCTCGGTGCTGAGGC 524
DB 61 GCACGAGGTGACGTGGCTGGGAGACACCTGGCCATGCTACTGAGCTCGGTGCTGAGGC 120
QY 525 AAGGCCCTCTTGGGAGACAGAGCCACCGGGGTGAGAGCTCTCGAGGTGGAGAG 584
DB 121 AAGGCCCTCTTGGGAGACAGAGCCACCGGGGTGAGAGCTCTCGAGGTGGAGAG 180
QY 585 CTTGGAGAAAGACGGCCACTTTTCAGAACATTGCTGGTCTCTGAAACCGGGAGGTGA 644
DB 181 CTTGGAGAAAGACGGCCACTTTTCAGAACATTGCTGGTCTCTGAAACCGGGAGGTGA 240
QY 645 GAGGGTGGCCATGACTGCCAGAGCCCTGACCGGCGAGCACCGGCTGGACCAAGAT 704
DB 241 GAGGGTGGCCATGACTGCCAGAGCCCTGACCGGCGAGCACCGGCTGGACCAAGAT 300
QY 705 TGAAGCCCTGAGTAGCAAGCTGCAGCAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGGC 764
DB 301 TGAAGCCCTGAGTAGCAAGCTGCAGCAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGGC 360
QY 765 GATGGCTGACTTGGAGCAGAAAGTCTTGGAGATGAGAGGATCCACCTCAAGTGGGTCTT 824
DB 361 GATGGCTGACTTGGAGCAGAAAGTCTTGGAGATGAGAGGATCCACCTCAAGTGGGTCTT 420
QY 825 CATCTGGAAGATCTCAGATTCGCCAGAGCTCCAGGAAGCTGTGGCTGGCCGATACC 884
DB 421 CATCTGGAAGATCTCAGATTCGCCAGAGCTCCAGGAAGCTGTGGCTGGCCGATACC 480
QY 885 CGCCATCTTCTCCCGAGCTTCTACACAGCAGGTACGGCTACAAGATGTGTCTGGGTAT 944
DB 481 CGCCATCTTCTCCCGAGCTTCTACACAGCAGGTACGGCTACAAGATGTGTCTGGGTAT 540
QY 945 CTACCTGAAACGGGAGACGGGACCGGAGGAGAAACACCTCTCTCTTTTGTGTGAT 1004
DB 541 CTACCTGAAACGGGAGACGGGACCGGAGGAGAAACACCTCTCTCTTTTGTGTGAT 600

QY 1005 GAAGGGCCCAATGACGCCCTGCTGGGTGGCCCTTCAACCAAGAGTGAC 1055
DB 601 GAAGGGCCCAATGACGCCCTGCTGGGTGGCCCTTCAACCAAGAGTGAC 651
RESULT 9
CD630730/c 666 bp mRNA linear EST 12-JAN-2004
LOCUS 56071275H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION 56071275H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630730
VERSION CD630730.1 GI:40278996
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 666)
AUTHORS Fu, G.X., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com
FEATURES
source
1..666
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
ORIGIN
Query Match 50.9%; Score 646.2; DB 6; Length 666;
Best Local Similarity 99.5%; Pred. No. 2.9e-145;
Matches 648; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 405 CCCTTCAGATTCCAGCCATCGGCTCGCTCGAGACGGTAGAGGTGAGAAACAGCAGGA 464
DB 666 CCCTTCAGATTCCAGCCATCGGCTCGCTCGAGACGGTAGAGGTGAGAAACAGCAGGA 607
QY 465 GCACGAGGTGAGTGGCTGGGAGACACCTGGCCATGCTACTGAGCTCGGTGCTGAGGC 524
DB 606 GCACGAGGTGAGTGGCTGGGAGACACCTGGCCATGCTACTGAGCTCGGTGCTGAGGC 547
QY 525 AAGGCCCTCTTGGGAGACAGAGCCACCGGGGTGAGAGCTCTCGAGAGGTGGAGAG 584
DB 546 AAGGCCCTCTTGGGAGACAGAGCCACCGGGGTGAGAGCTCTCGAGAGGTGGAGAG 487
QY 585 CTTGGAGAAAGACGGCCACTTTTGAGAACATTGCTGGCTCTGAAACCGGGAGGTGA 644
DB 486 CTTGGAGAAAGACGGCCACTTTTGAGAACATTGCTGGCTCTGAAACCGGGAGGTGA 427
QY 645 GAGGGTGGCCATGACTGCCAGGCTCGGAGGCTGAGCCGAGCACCGGCTGGACCAAGAT 704
DB 426 GAGGGTGGCCATGACTGCCAGGCTCGGAGGCTGAGCCGAGCACCGGCTGGACCAAGAT 367
QY 705 TGAAGCCCTGAGTAGCAAGTCTTGGAGATGAGAGGATTTGGCTCAAGGACCTGGC 764
DB 366 TGAAGCCCTGAGTAGCAAGTCTTGGAGATGAGAGGATTTGGCTCAAGGACCTGGC 307
QY 765 GATGGCTGACTTGGAGCAGAAAGTCTTGGAGATGAGAGGATCCACCTCAAGTGGGTCTT 824
DB 306 GATGGCTGACTTGGAGCAGAAAGTCTTGGAGATGAGAGGATCCACCTCAAGTGGGTCTT 247
QY 825 CATCTGGAAGATCTCAGACTTCGCCAGAGCTCCAGGAAGCTGTGGCTGGCCGATACC 884
DB 246 CATCTGGAAGATCTCAGACTTCGCCAGAGCTCCAGGAAGCTGTGGCTGGCCGATACC 187
QY 885 CGCCATCTTCTCCCGAGCTTCTACACAGCAGGTACGGCTACAAGATGTGTCTGGGTAT 944

Db 186 CCGCATCTTCTCCCGAGCCTTCTACACAGCAGGATACGGCTACAGATGTGTGTGCGTAT 127

QY 945 CTACCTGAACGGCGACGGCGCGGAGGAAACACACCTGTCCCTCTCTCTTTGTGGTGAT 1004

Db 126 CTAACCTGAACGGCGACGGCGCGGAGGAAACACACCTGTCCCTCTCTTTGTGGTGAT 67

QY 1005 GAAGGGCCGAATGACGGCCCTGCTCGGTGGCCCTTCAACAGAGAGTGAC 1055

Db 66 GAAGGGCCGAATGACGACCTGCTCGGTGGCCCTTCAACAGAGTGAC 16

RESULT 10

BU857656

LOCUS

DEFINITION

AGENCOURT_10474335 NIH_MGC_107 Homo sapiens cDNA clone

IMAGE:6647537 5', mRNA sequence.

BU857656

VERSION

EST.

BU857656.1 GI:24042648

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

1. (bases 1 to 934)

1. NIH-MGC http://mgc.nci.nih.gov/

2. National Institutes of Health, Mammalian Gene Collection (MGC)

3. Unpublished (1999)

4. Contact: Robert Strausberg, Ph.D.

5. Email: cgapbs-remail.nih.gov

6. Tissue Procurement: ATCC

7. cDNA Library Preparation: Rubin Laboratory

8. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

9. DNA Sequencing by: Agencourt Bioscience Corporation

10. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

11. Plate: L1CM2888 row: b column: 17

12. High quality sequence stop: 659.

13. Location/Qualifiers

1. .934

2. organism="Homo sapiens"

3. mol_type="mRNA"

4. db_xref="taxon:9606"

5. /clone="IMAGE:6647537"

6. /tissue_type="adenocarcinoma, cell line"

7. /lab_host="DH10B (phage-resistant)"

8. /clone_lib="NIH_MGC_107"

9. /note="Organ: breast; Vector: pOTB7; Site: 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 49.8%; Score 631.4; DB 5; Length 934;

Best Local Similarity 99.8%; Pred. No. 1.2e-141;

Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 637 GAGTGGAGAGGGTGGCCATGATGCCGAGCGCTGACCGGCGAGCACCGGCTGGACCAA 696

Db 1 GAGTGGAGAGGGTGGCCATGATGCCGAGCGCTGACCGGCGAGCACCGGCTGGACCAA 60

QY 697 GACAAGATTGAGCCCTGAGTACGAGTGCAGAGTGGAGAGGAGGATGGCCCTCAAG 756

Db 61 GACAAGATTGAGCCCTGAGTACGAGTGCAGAGTGGAGAGGAGGATGGCCCTCAAG 120

QY 757 GACTGGCGATGGCTGATGGAGCAGAGAGGCTTGGAGATGGAGGCATCCACCTACGAT 816

Db 121 GACTGGCGATGGCTGATGGAGCAGAGAGGCTTGGAGATGGAGGCATCCACCTACGAT 180

QY 817 GGGGTCTTTCATCTCGAAGATCTCAGACTTCGCGAGGAAGCTCCAGGAGCTGTGGCTGCG 876

Db 181 GGGGTCTTTCATCTCGAAGATCTCAGACTTCGCGAGGAAGCTCCAGGAGCTGTGGCTGCG 240

QY 877 CGCATACCCGCCATCTTCTCCCGAGCTTCTACCCAGCAGGTACGGCTACAGATGTGT 936

Db 241 CGCATACCCGCCATCTTCTCCCGAGCTTCTACCCAGCAGGTACGGCTACAGATGTGT 300

QY 937 CTGCGTATCTACTGAAACGGCGACGCGCGGCGAGGACACACCTGTCCCTCTTCTTT 996

Db 301 CTGCGTATCTACTGAAACGGCGACGCGCGGCGAGGACACACCTGTCCCTCTTCTTT 360

QY 997 GTGGTGAAGAGCGCCGAATGACGCGCTTCTGCGGTGGCCCTTCAACAGAGGTGACC 1056

Db 361 GTGGTGAAGAGCGCCGAATGACGCGCTTCTGCGGTGGCCCTTCAACAGAGGTGACC 420

QY 1057 TTAATGCTCTCGACCAAGTAACCGGAGGACGAGTGAAGCCCTTACGGCCCGACGTG 1116

Db 421 TTAATGCTCTCGACCAAGTAACCGGAGGACGAGTGAAGCCCTTACGGCCCGACGTG 480

QY 1117 ACTTCATCTCTTTTTCAGAGGCGCAGTCAACGACATGAACATCGAAGCGGCTGCCCTTC 1176

Db 481 ACTTCATCTCTTTTTCAGAGGCGCAGTCAACGACATGAACATCGAAGCGGCTGCCCTTC 540

QY 1177 TTCTGCCCCGTCTCAAGATGGAGCAAGAAATTCCTACGTGCGGAGCGATGCCATCTTC 1236

Db 541 TTCTGCCCCGTCTCAAGATGGAGCAAGAAATTCCTACGTGCGGAGCGATGCCATCTTC 600

QY 1237 ATCAAGGCGCATTTGCGACTGACAGCGCTCTAA 1269

Db 601 ATCAAGGCGCATTTGCGACTGACAGCGCTCTAA 633

RESULT 11

BU513753

LOCUS

DEFINITION

AGENCOURT_10118304 NIH_MGC_134 Mus musculus cDNA clone

IMAGE:8510327 5', mRNA sequence.

BU513753

VERSION

EST.

BU513753.1 GI:22821279

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

1. (bases 1 to 937)

1. NIH-MGC http://mgc.nci.nih.gov/

2. National Institutes of Health, Mammalian Gene Collection (MGC)

3. Unpublished (1999)

4. Contact: Robert Strausberg, Ph.D.

5. Email: cgapbs-remail.nih.gov

6. Tissue Procurement: Dr. David Rowe

7. cDNA Library Preparation: Invitrogen Corp

8. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

9. DNA Sequencing by: Agencourt Bioscience Corporation

10. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

11. Plate: L1CM14079 row: a column: 16

12. High quality sequence stop: 648.

13. Location/Qualifiers

1. .937

2. organism="Mus musculus"

3. mol_type="mRNA"

4. db_xref="taxon:10090"

5. /clone="IMAGE:8510327"

6. /tissue_type="undifferentiated limb"

7. /lab_host="DH10B (phage-resistant)"

8. /clone_lib="NIH_MGC_134"

9. /note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."

FEATURES

source


```
ORIGIN
Query Match      45.5%; Score 577.2; DB 5; Length 937;
Best Local Similarity 80.3%; Pred. No. 1.5e-128;
Matches 689; Conservative 0; Mismatches 168; Indels 1; Gaps 1;

QY 366 GTTTCAGGACCAAGTCAAGACTGTGGCAAGTGTGAGTCCCTTCAGATTCACCGCAT 425
DB 45 GTTTCAGGACCAAGTGTAGAGCATGACGAAATGCGGGTCTCTGAGATTCACCGCAT 104

QY 426 CGGCTCCCTCGAGACGGTGTAGAGGTTGAGAAACAGCAGGACGAGGTGCAGTGTGG 485
DB 105 TGGCTGTTTCAGAGATGTTGAGACTGAGAACTGAGAGATCATGAGTGCACGGCTAG 164
QY 486 GAGACCTCGGCATCTACTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545
DB 165 GGAACACCTAGCCCTACTGCTGAGCTCACTTCTTGGAGGCCCAAGCCTCTCCAGGAACCTT 224
QY 546 GAGCCACGGGGTTCAGAGCTCTGCTGAGAGGTGCGAGAGCTGGAGAAAGAACAGCCAC 605
DB 225 GAACAGGTGGGCGAGAGTACTCTAGCGGTGCCAGATTTTGGAGCAGAGATAGCAAC 284
QY 606 TTTTGAGAACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
DB 285 CTTTGAGAACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344
QY 666 GGCCTCCAGCCGACACCGCTGCAACCAAGACAGATTTGAAGCCTGAGTAGCAAGT 725
DB 345 GGTCTGAGCGGACACCGCTGACAGCAAGATTTGAGCCCTGAGTAAAGT 404
QY 726 GCACAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGGCGATTTGGTGAATTTGGAGCAGAA 785
DB 405 GCAACAGCTGGAGAGGAGCATGGCTCAAGGACCTGGCGATTTGGTGAATTTGGAGCAGAA 464
QY 786 GGTCTTGGAGATGGAGCATCTACCTACAGTGGGTCTTCATCTGGAAGATCTCAGACTT 845
DB 465 GGTCTCCGAGTTGGAAGTATCCACCTATGATGGGGTCTTCATCTGGAAGATCTCAGACTT 524
QY 846 CGCCAGAGCTCCAGAGAGCTGTGCTGCGCCGATACCGCCATCTTCTCCCGAGCCCT 905
DB 525 CACCAAGAGCTCAGAGAGCTAGCTGGCCGACACCAAGCTATCTTCTCCCGAGCCCT 584
QY 906 CTACACAGCAGTACGGGTACAGATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 965
DB 585 CTACACAGCAGATATGGCTTACAGATGTCTTACGAGTCTACTTGAATGGGCGAGCCAC 644
QY 966 CGGCGAGGAGACACACTGCTGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1025
DB 645 TGGCGGGGAACTCATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 704
QY 1026 GCTCGGCTGGCCCTTCAACAGAGGTGACCTTTAATGCTGCTGCTGCTGCTGCTGCTGCT 1085
DB 705 GTTGCAGTGGCTTTTAAATCAGAAAGGTAAATGATGTTGCTGGGACATAACCCCGGGA 764
QY 1086 GCAGTGATTTAGCCCTTACGCGCCGACGAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1145
DB 765 GCATGTGATCGAGCATTCAGGCGCGATGATGATGATGATGATGATGATGATGATGATGAT 924
QY 1146 CGACATGAACATCG-CAAGCGGCTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1204
DB 825 TGACATGAACATCGCCAGTGGCTTGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 884
QY 1205 AGAATTCCTAGTGGCGG 1222
DB 885 AGAATTCCTATGGGCGG 902

RESULT 12
BM790399
LOCUS      578 bp      mRNA      linear      EST 05-MAR-2002
DEFINITION K-EST0070221 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-8-D01
5', mRNA sequence.
ACCESSION BM790399
```

```
BM790399.1 GI:19138631
EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 578)
AUTHORS     Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE       21C Frontier Korean EST Project 2001
JOURNAL      Unpublished (2002)
COMMENT      Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 8 row: D column: 01
            High quality sequence stop: 578.
FEATURES     Location/Qualifiers
             1..578
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="S22SNU16n1-8-D01"
                /sex="F"
                /tissue_type="Ascites"
                /cell_type="Lymphoblast-like"
                /lab_host="SNU-16"
                /clone_lib="S22SNU16n1"
                /note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI;
                Site 2: NotI; The S22SNU16 library was contributed by the
                Soares laboratory and it was constructed as described by
                Soares, M.F., Lennon, G. and Soares, M.B. (1996) Genome
                Research 6(9): 791-806. RNA was prepared from harvested
                cells of SNU-16 culture. SNU-16 cell was established from
                Korean Cell Line Bank (KCLB). SNU-16 was established from
                ascitic fluids of Korean patients by Park J.G. et al.
                (1990), Cancer Res 50: 2773-2780."
ORIGIN
Query Match      45.2%; Score 573.2; DB 4; Length 578;
Best Local Similarity 99.5%; Pred. No. 1.3e-127;
Matches 575; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 629 TGAACCGGAGGTGAGAGGTGGCCATGACTGCGAGGCTGCGAGCGGAGCAGCCGGC 688
DB 1 TGAACCGGAGGTGAGAGGTGGCCATGACTGCGAGGCTGCGAGCGGAGCAGCCGGC 60
QY 689 TGGACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCAGCAGCTGGAGAGGAGCATTT 748
DB 61 TGGACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCAGCAGCTGGAGAGGAGCATTT 120
QY 749 GCCTCAAGAGCTGGCGATGCTGACTTGGAGCAGAGGTCTTGGAGATGAGGAGCATCCA 808
DB 121 GCCTCAAGAGCTGGCGATGCTGACTTGGAGCAGAGGTCTTGGAGATGAGGAGCATCCA 180
QY 809 CCTACGATGGGCTCTTCACTCTGGAAGATCTCAGACTTGGCCAGGAAGTCCAGGAAGCTG 868
DB 181 CCTACGATGGGCTCTTCACTCTGGAAGATCTCAGACTTGGCCAGGAAGTCCAGGAAGCTG 240
QY 869 TGGCTGGCGGATACCCCGCATCTTCTCCAGCCTTCTACACGAGAGGTACGGCTACA 928
DB 241 TGGCTGGCGGATACCCCGCATCTTCTCCAGCCTTCTACACGAGAGGTACGGCTACA 300
QY 929 AGATGTGTCTGGTATCTACCTGAACGGCGAGCGCACCGGGCGAGGAACACACCTGTCCC 988
DB 301 AGATGTGTCTGGTATCTACCTGAACGGCGAGCGCACCGGGCGAGGAACACACCTGTCCC 360
QY 989 TCTTCTTTTGTGTGATGAAGGGCCCGCCCTCTCTGGGTGGCCCTTCAACACAGA 1048
```

```

Db      361  TCTTCTTTGCTGATGAAGGCGCGAATGAGCCCTGCTGGGTGGCCCTTCAACCA 420
Qy      1049  AGGTGACCTTAATGCTGCTGCAACGAATAACCGGAGACAGTGAATGACGCCCTTCAGGC 1108
Db      421  AGGTGACCTTAATGCTGCTGCAACGAATAACCGGAGACAGTGAATGACGCCCTTCAGGC 480
Qy      1109  CCGAGCTGACTTCATCTCTTTTCAGAGCCAGTCAACGACATGAACATCCAGAGCGCT 1168
Db      481  CCGAGCTGACTTCATCTCTTTTCAGAGCCAGTCAACGACATGAACATCCAGAGCGCT 540
Qy      1169  GCCCCTCTTCTGCCCCGCTCCCAAGATGGAGGCAAG 1206
Db      541  GCCCCTCTTCTGCCCCGCTCCCAAGATGGAGGCAAG 578

RESULT 13
LOCUS   AY413599
DEFINITION Pan troglodytes TRAF2 gene, linear GSS 17-DEC-2003
GENOMIC SURVEY SEQUENCE
ACCESSION AY413599.1 GI:39769561
KEYWORDS VERSION
SOURCE GSS.
ORGANISM Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1335)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submision
JOURNAL Submitted (18-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..1335
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1335
/gene="TRAF2"
/locus_tag="HGM4944"
gene
ORIGIN
Query Match 39.3%; Score 498.6; DB 9; Length 1335;
Best Local Similarity 56.0%; Pred. No. 1.6e-109;
Matches 748; Conservative 0; Mismatches 350; Indels 237; Gaps 1;
Qy      23  CCCCTGGCTCCCTGGAGTGTGTACAGCCGGCTTCTCCAGAGCCCTCCCTGGGACCAAGC 82
Db      1  CCCCTGGCTCCCTGGAGTGTGTACAGCCGGCTTCTCCAGAGCCCTCCCTGGGACCAAGC 60
Qy      83  TGGAGCCAGTACTGTGCTCCGCTTGCAGAAACGTCCTCCGACGCGCTTCAGGCGC 142
Db      61  TGGAGCCAGTACTGTGCTCCGCTTGCAGAAACGTCCTCCGACGCGCTTCAGGCGC 120
Qy      143  AGTGTGCCACCGGTACTGTCTTCTGCTGGCCAGCATCTCAGCTCTGGGCGCTCAGA 202
Db      121  AGTGTGCCACCGGTACTGTCTTCTGCTGGCCAGCATCTCAGCTCTGGGCGCTCAGA 180

```

```

Qy      203  ACTGTGCTGCTGCTGTTTCAAGAGGCGATATATGAAGAGGCAATTTCTATTTTAGAAAGCA 262
Db      181  ACTGTGCTGCTGCTGTTTCAAGAGGCGATATATGAAGAGGCAATTTCTATTTTAGAAAGCA 240
Qy      263  GTTTCGGCCTTCCAGATAATGCTGCCCGCAGGAGGTGGAGAGCCTGCCGCGCCTGCTGTC 322
Db      241  GTTCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 300
Qy      323  CAGTGAATGATGCACTGGAAGGGGACCTCGAAGAAATACG----- 364
Db      301  CCAGTGAATGATGCACTGGAAGGGGACCTCGAAGAAATACGAGAGCTGCCACAGGGGCC 360
Qy      365  ----- 364
Db      361  GCTGCCCGCTCATGCTGACTGAATGTCCCGCGTCAAGAGGCTGGTCCGCGCTTGGTGAAA 420
Qy      365  ----- 364
Db      421  AGGAGCGCCACCTGGAGCACGAGTGCCTGGAGAGAACCTGAGCTGCCGGCATTGCCGGG 480
Qy      365  ----- 364
Db      481  CGCCCTGCTGCGGAGCAGAGCTGAAGGGCGCACCCAGAGTCTGCCCCCAAGTTTCCCTTAA 540
Qy      365  -----AGTTTCAGGACCAACGCTCAAGA 385
Db      541  CTTGTGACGGCTGCGGCAAGAAAGATCCCGCGGAGAGATTTCAGGACCAACGCTCAAGA 600
Qy      386  CTTGTGGCAAGTGTGAGTCCCTTCAGATTCCAGCCATCGGCTGCTCGAGACGGTAG 445
Db      601  CTTGTGGCAAGTGTGAGTCCCTTCAGATTCCAGCCATCGGCTGCTCGAGACGGTAG 660
Qy      446  AGGGTGAGAAACAGCAGGAGCACGAGTGCAGTGGCTGCGGAGCACCTGGCCATGCTAC 505
Db      661  AGGGTGAGAAACAGCAGGAGCACGAGTGCAGTGGCTGCGGAGCACCTGGCCATGCTAC 720
Qy      506  TGAGTCTGGTGTGAGGCAAGCCCTCTTGGGAGACAGAGCCACCGGGGTGAGAGC 565
Db      721  TGAGTCTGGTGTGAGGCAAGCCCTCTGCGGAGACAGAGCCACCGGGGTGAGAGC 780
Qy      566  TCCTCAGAGGTGCGAGAGCCTGGAGAGAGAGAGCGCCATTTTGAGAACATGCTGCG 625
Db      781  TCCTCAGAGGTGCGAGAGCCTGGAGAGAGAGAGCGCCATTTTGAGAACATGCTGCTG 840
Qy      626  TCCTGAACCGGAGGTGGAGAGGTGGCCATGACTGCGAGGCGCTGAGCCGCGGAGCACC 685
Db      841  TCCTGAACCGGAGGTGAGAGGTGGCCATGACTGCGAGGCGCTGAGCCGCGGAGCACC 900
Qy      686  GGCTGGACCAAGACAGATTGAAGCCCTGAGTAGCAAGGTGCAGCTGGAGAGGAGCA 745
Db      901  GGCTGGACCAAGACAGATTGAAGCCCTGAGTAGCAAGGTGCAGCTGGAGAGGAGCA 960
Qy      746  TTGGCCTCAAGGACCTGCGGATGCTGACTTGGAGAGAGAGGTCTTGGAGATGGAGGCAT 805
Db      961  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1020
Qy      806  CCACCTACATGGGGTCTTCACTTGGAGAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAG 865
Db      1021  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1080
Qy      866  CTGTGGCTGGCGCATACCGCCCATCTTCTCCAGCCCTTCAACAGCAGGATGACGGCT 925
Db      1081  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1140
Qy      926  ACAAGATGTGCTGCGTATCTACTGAACGCGGACGGCAACCGGCGAGGAGCAACACCTGT 985
Db      1141  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1200
Qy      986  CCCTCTTCTTTGTGTGATGAAGGGCCGCAATGACGCGCTGCTGCGGTGGCCCTTCAACC 1045
Db      1201  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1260
Qy      1046  AGAAGGTGACCTTAATGCTGCTGCACAGAAATAACCGGGAGCAGCTGATGTTGACGCTTCA 1105

```

```

Db      1261 NNNNGTGACCTTAATGCTCTCGACAGATAAACCAGGACGCGATTGACGCGCTTCA 1320
Qy      1106 GGCCCGACGTGACTT 1120
Db      1321 GGCCCGACGTGACTT 1335

RESULT 14
LOCUS   CK596664
DEFINITION AGENCOURT 17837571 NIH MGC 238 Rattus norvegicus cDNA clone
IMAGE: 7131710 5', mRNA sequence.
ACCESSION CK596664
VERSION    CK596664.1 GI:41109747
KEYWORDS  EST.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 710)
          NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics / NIH
          National Cancer Institute
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgabs-k@mail.nih.gov
          Tissue Procurement: Howard Jacobs
          cDNA Library Preparation: Express Genomics
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM15032 row: p column: 12
          High quality sequence stop: 585.
FEATURES             source
     1..710
     /organism="Rattus norvegicus"
     /mol_type="mRNA"
     /db_xref="taxon:10116"
     /clone="IMAGE:7131710"
     /tissue_type="testis, pooled"
     /lab_host="DH10B TONa"
     /clone_11b="NIH_MGC_238"
     /note="Organ: testis; Vector: pExpress-1; Site: 1: EcoRV;
     Site 2: NotI; RNA obtained from testis tissue of 8 wk old
     animal. Tissues were snap-frozen and kept at -80C before
     RNA extraction and purification (Tri-reagent method). cDNA
     was primed using oligo-dT primer:
     5'-pGACTAGTCTAGATCGGAGCGCGCCGCTT-3' and cloned into
     the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
     resulted in an average insert size of 1.9 kb. This primary
     library is normalized (non-normalized primary library is
     NIH MGC 237) and was constructed by Express Genomics
     (Frederick, MD)"
ORIGIN
Query Match      38.5%; Score 488; DB 7; Length 710;
Best Local Similarity 84.3%; Pred. No. 5.3e-107;
Matches 573; Conservative 0; Mismatches 105; Indels 2; Gaps 2;

Qy      555 GGCGTCAGAGCTCCTCGAGAGGTGCGAGAGCTGGAGAGAGACGGCCACTTTTGAGAA 614
Db      2 GGCGCCAGAGCTGTTACAGCGGTGCCAGATTGGAGCAGAGAGATAGCCACTTTGAGNA 61.

Qy      615 CATTTGCTCGGTCCTGAACCGGAGGTGGAGAGGGTGGCCATGACTGCGAGGCGCTTGCAG 674
Db      62 CATTTGCTCGGTTTGAACCGGAGGTAGAGAGGGTAGCAGTGAATGCTGACGAGGCTTGTAG 121

```

```

Qy      675 CCGCAGACCCGGCTGGACCAAGAACAAGATTGAAGCCCTGAGTAGCAAGGTGCGACGACT 734
Db      122 CCGCAGACCCGGCTGAGACCAAGGACAAGATTGAGCCCTTAAGCAACAAGGTGCGACGACT 181
Qy      735 GGAGAGGAGCATTGGCCCTCAAGGACCTGGCGATGGCTGACTTGGAGCAGAGAGGTCTTGA 794
Db      182 GGAGAGGAGCATTGGCCCTCAAGGACCTGGCCATGGCTGACTGAGCAGAGAGGTCTTGA 241
Qy      795 GATGAGGAGCATCCACCTACGATGGGGTCTTCATCTGGAAGATCTCAGACTTTCGACAGAA 854
Db      242 GTTGGAGGTGCCACCTATGATGGGTCTTTCATCTGGAAGATCTCCGACTTCGACAGAA 301
Qy      855 GCTCCAGGAAGCTGTGGCTGGCGCATACCGCCATCTTCTCCCGACGCTTCTACACAG 914
Db      302 ACGTCAGGAAGCATGCGCTGGCGGACACCTGCTATCTTCTCCCGACGCTTCTTCAAG 361
Qy      915 CAGGTACGGCTACAGATGTGTCTGCGCTATCTACTGAACGGCGACGCGACGGCGGAGG 974
Db      362 CAGATATGGCTACAAGATGTGTCTCCGGGTCTACTTGAATGGCGACGCGACTGGGCGGG 421
Qy      975 AACACACCTGTCCCTCTTCTTTGGTGTGATGAAGGGCCGGAATGACGCCCTGCTGGGTG 1034
Db      422 AACTCATCTGTCTCTCTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 481
Qy      1035 GCCCTTCAACAGAGAGGTGACCTTAAATGCTGCTCGACAGATAAACCGGAGGACGCTGAT 1094
Db      482 GCCCTTCAACAGAGAGGTGACCTTAAATGCTGCTCGACAGATAAACCGGAGGACGCTGAT 541
Qy      1095 TGAGCCTTACAGGCGGACGAGTCACTTCACTCTTTTTCAGAGGCGGACGACGATGAA 1154
Db      542 CGAGCATTTACAGGCGGCTGATTAACCTTCTGCTCTCCAGAGGCGCTGCTGAGTGAATGAA 601
Qy      1155 CATGCGAGCGGCTGCCCGCTCTCTGCGCGCTCTCCAGATGAGGACGAGGATTCCTA 1214
Db      602 TATGCGCAGTGGTGGCGCGCTCTCTGCGCGGTGTC-AGATAGAGCCAGAAATT-CTA 659
Qy      1215 CGTGGGAGCATGCCATCT 1234
Db      660 CGTGGGAGCATGCCATCT 679

RESULT 15
AW882089
LOCUS   AW882089
DEFINITION RC6-OT0050-230200-021-B06 OT0050 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW882089
VERSION   AW882089.1 GI:8044099
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 495)
          Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
          Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
          Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
          Brunstein, A., Golliveira, P.S., Bucher, P., Jongeneel, C.V.,
          O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
          Simpson, A.J.
          Shotgun sequencing of the human transcriptome with ORF expressed
          sequence tags
          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
          MEDLINE 20202663
          PUBMED 10737800
          COMMENT
          Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome

```

Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC6-OT0050-230
 200-021-B06&t3=2000-02-23&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 9
 High quality sequence stop: 397.
 Location/Qualifiers
 1. .495

FEATURES

source
 1. .495
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="OT0050"
 /note="Organ: ovary; Vector: puc18; Site 1: SmaI; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN

Query Match	38.3%	Score 486.2;	DB 2;	Length 495;
Best Local Similarity	99.2%	Pred. No. 1.4e-106;		
Matches 488;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

QY 632 ACCGGAGGTGGAGAGGTGGCCATGACTGCCGAGGCTGCGCCGAGCGGCTGG 691
 DB 4 ACCGAGAGGTGGAGAGGTGGCCATGACTGCCGAGGCTGCGCCGAGCGGCTGG 63
 QY 692 ACCAGACAAAGTTCAAGCCCTGAGTACAGAGTGCACAGCTGCGAGAGGATGGCC 751
 DB 64 ACCAGACAAAGTTCAAGCCCTGAGTACAGAGTGCACAGCTGCGAGAGGATGGCC 123
 QY 752 TCAAGGACCTGGCGATGGCTGACTTGGAGCAGAAGGTCTTGGAGATGGAGGCATCCACCT 811
 DB 124 TCAAGGACCTGGCGATGGCTGACTTGGAGCAGAAGGTCTTGGAGATGGAGGCATCCACCT 183
 QY 812 ACGATGGGGTCTTCATCTGGAGATCTCAGACTTGGCCAGGAGCTCCAGGAGCTGTGG 871
 DB 184 ACGATGGGGTCTTCATCTGGAGATCTCAGACTTGGCCAGGAGCTCCAGGAGCTGTGG 243
 QY 872 CTGGCCGCATACCCGCCATCTTCTCCCGAGCTTCTACACAGCAGGTACGGCTACAAGA 931
 DB 244 CTGGCCGCATACCCGCCATCTTCTCCCGAGCTTCTACACAGCAGGTACGGCTACAAGA 303
 QY 932 TGTGTCTCGGTATCTACCTGAACCGGACGCGACCGGGCGAGGAAACACACTGTCTCCCTCT 991
 DB 304 TGTGTCTCGGTATCTACCTGAACCGGACGCGACCGGGCGAGGAAACACACTGTCTCCCTCT 363
 QY 992 TCTTTGTGGTGAAGGGCCCGGATGACGCCCTGCTGGGTGGCCCTTCAACCCAGAGG 1051
 DB 364 TCTTTGTGGTGAAGGGCCCGGATGACGCCCTGCTGGGTGGCCCTTCAACCCAGAGG 423
 QY 1052 TGACCTTAATGCTGCTCGACAGAAATACCCGGAGCAGTGAATGAGCCCTTCAGGCCCG 1111
 DB 424 TGACCTTAATGCTGCTCGACAGAAATACCCGGAGCAGTGAATGAGCCCTTCAGGCCCG 483
 QY 1112 ACGTGACTTCAT 1123
 DB 484 ACGTGACTTCAT 495

Search completed: November 6, 2004, 22:02:17
 Job time : 4410 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2004, 16:10:49 ; Search time 155 Seconds
(without alignments)
976.669 Million cell updates/sec

Title: US-10-018-030b-2

Perfect score: 2211

Sequence: 1 MAASVTPGSELQPGFS.....NSVYRDAIFKAVDLTGL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Genesep238ep04:*
2: Genesep1980s:*
3: Genesep1990s:*
4: Genesep2000s:*
5: Genesep2001s:*
6: Genesep2002s:*
7: Genesep2003as:*
8: Genesep2003bs:*
9: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2211	100.0	422	AAy71901	AAy71901 Human TRA
2	2047.5	92.6	501	AAy98165	AAy98165 Human TRA
3	2047.5	92.6	501	AAy71903	AAy71903 Human TNF
4	2047.5	92.6	501	ABO07170	ABO07170 Human p53
5	2047.5	92.6	501	ADB80956	ADB80956 RING-SH C
6	2047.5	92.6	501	ABR4599	ABR4599 TRAF2 pro
7	2047.5	92.6	501	ADM45822	ADM45822 TNF-alpha
8	1914.5	86.6	501	ABBS7335	ABBS7335 Mouse isc
9	1909.5	86.4	501	AAr90578	AAr90578 Mouse TRA
10	1751	79.2	336	AAy71902	AAy71902 Human TRA
11	1631.5	73.8	447	ADA54134	ADA54134 Human pro
12	1178	53.3	243	ABO7002	ABO7002 Human TRA
13	999.5	45.2	326	ABU70784	ABU70784 Human adi
14	733.5	33.2	416	AAW03147	AAW03147 Epstein-B
15	733.5	33.2	416	AAy98164	AAy98164 Human TRA
16	733.5	33.2	416	ADF76476	ADF76476 Novel hum
17	733.5	33.2	416	ADL22912	ADL22912 Human MP2
18	733.5	33.2	416	ADL82947	ADL82947 Human PRO
19	733.5	33.2	416	ADO20499	ADO20499 Human PRO
20	733.5	33.2	416	ADO19524	ADO19524 Human PRO
21	730	33.0	567	AAO17756	AAO17756 Murine CD
22	727	32.9	409	AAr90577	AAr90577 Human TRA
23	722	32.7	543	AAW27432	AAW27432 Human TRA
24	722	32.7	543	ABO07169	ABO07169 Human p53
25	722	32.7	665	AAW27433	AAW27433 Human TRA

26	721.5	32.6	516	2	AAW27436	Human CRA
27	721.5	32.6	638	2	AAW27437	Human CRA
28	719	32.5	567	5	ABBS7054	Mouse isc
29	717.5	32.5	568	2	AAW27431	Human CRA
30	717.5	32.5	568	3	AAy98166	Human TRA
31	717.5	32.5	568	5	AAO17757	Human CD4
32	717.5	32.5	568	7	ADB80964	RING-SH C
33	717.5	32.5	568	7	ADB80957	RING-SH C
34	717.5	32.5	690	2	AAW27428	Human CRA
35	717	32.4	543	2	AAr98833	CD40 asso
36	713.5	32.3	568	2	AAW03146	LMP1 asso
37	713.5	32.3	568	6	ABO07171	Human p53
38	710.5	32.1	512	2	AAW27434	Human CRA
39	710.5	32.1	634	2	AAW27435	Human CRA
40	710	32.1	567	2	AAr99259	Full-leng
41	710	32.1	567	4	AAAB67615	Amino aci
42	710	32.1	567	7	ADD25542	Binding d
43	687.5	31.1	538	6	ABU89708	Protein d
44	687.5	31.1	557	2	AAW29258	Human TRA
45	687.5	31.1	557	2	AAW27610	Human TRA

ALIGNMENTS

RESULT 1

AAy71901

ID AAy71901 standard; protein; 422 AA.

XX

AC AAy71901;

DT 26-MAR-2001 (first entry)

XX

DE Human TRAF2 splice variant TRAF2TR (TRAF2 truncated) protein.

XX

KW Human; tumour necrosis factor; TNF; TRAF2-FL; inhibitor; treatment;

KW TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;

KW antiinflammatory; cardiant; myocardial infarction; splice variant;

KW vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;

KW antitumor sclerotic; immunosuppressive; Crohn's disease; psoriasis;

KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;

KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;

XX neurodegenerative disease.

XX OS Homo sapiens.

XX

PN WO200066737-Al.

XX

PD 09-NOV-2000.

XX

PF 06-APR-2000; 2000WO-US009178.

XX

PR 30-APR-1999; 99US-0131940P.

XX

PA (AVET) AVENTIS PHARM PROD INC.

XX

XX Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;

XX

DR WPI: 2001-007223/01.

XX

DR N-PSDB; AAO1947.

XX

PT New nucleic acid encoding variants of tumor necrosis factor receptor

PT associated factors useful for inhibiting tumor necrosis factor alpha-

PT regulated pathways, and for treating Crohn's disease, psoriasis, and

PT rheumatoid arthritis.

XX

PS Claim 5; Fig 2b; 74pp; English.

XX

CC The present sequence is a tumour necrosis factor (TNF)-receptor

CC associated factor-truncated (TRAF2TR) protein which inhibits TNF alpha-

CC regulated pathways. This sequence is a natural splice variant of human

CC TRAF2-FL (full-length) protein. The TRAF2TR variant is useful for

CC inhibiting diseases involving overproduction of TNFalpha, TNFalpha

QY 402 KNSVVRDDAIFIKAIIVDLTGL 422
 Db 481 KNSVVRDDAIFIKAIIVDLTGL 501

RESULT 3
 AAY71903
 ID AAY71903 standard; protein; 501 AA.
 AC AAY71903;
 XX DT 26-MAR-2001 (first entry)
 XX DE Human TNF-receptor associated factor (TRAF2) protein.
 XX KW Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
 KW TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
 KW TRAF2 truncated-deleted; TRAF2TD; antiinflammatory; cardiac; vasotropic;
 KW antiapoptotic; antirheumatic; antiarthritic; antidiabetic;
 KW antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
 KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;
 KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
 KW neurodegenerative disease.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Region 2..87
 FT /note= "This region is absent in TRAF2TD (AAY71902)"
 FT Region 123..201
 FT /note= "This region is absent in TRAF2TR (AAY71901) and
 TRAF2TD (AAY71902)"
 XX WO200066737-A1.
 XX PD 09-NOV-2000.
 XX PF 06-APR-2000; 2000WO-US009178.
 XX PR 30-APR-1999; 99US-0131940P.
 XX PA (AVET) AVENTIS PHARM PROD INC.
 XX PI Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
 XX WPI: 2001-007223/01.
 XX N-PSDB; AAD01949.
 XX PT New nucleic acid encoding variants of tumor necrosis factor receptor
 associated factors useful for inhibiting tumor necrosis factor alpha-
 regulated pathways, and for treating Crohn's disease, psoriasis, and
 rheumatoid arthritis.
 XX PS Example 1; Fig 4b; 74pp; English.
 XX CC The present sequence is human tumour necrosis factor (TNF)-receptor
 associated factor-full length (TRAF2-FL) protein. TRAF2-FL has two
 variants, a splice variant of TRAF2 referred as "TRAF2 truncated"
 (TRAF2TR) and a TRAF2 expression construct with enhanced dominant
 negative properties referred as "TRAF2 truncated-deleted" (TRAF2TD).
 CC TRAF2-TR and TRAF2-TD are also capable of inhibiting TNF alpha signalling
 pathways. The TRAF2 variants are useful for inhibiting diseases involving
 over production of TNFalpha, TNFalpha pathologies involving
 hyperactivation of nuclear factor kappa B (NFkB). The variants are also
 useful for inhibiting and treating inflammatory processes involving
 TNFalpha such as Crohn's disease, psoriasis, rheumatoid arthritis, graft
 versus host disease, non-insulin dependent diabetes, inflammatory bowel
 disease, and neurodegenerative diseases or cardiovascular disease such as
 cardiac ischaemia-reperfusion injury following myocardial infarction,
 coronary artery bypass surgery, cardiac transplantation or ischaemia-
 reperfusion injury in the central nervous system (CNS) following stroke,
 the progression and rupture of advanced coronary atherosclerotic plaques,

CC development and progression of congestive heart failure, endothelial cell
 CC injury following balloon angioplasty, or apoptotic cell death of
 CC myocardial cells
 XX Sequence 501 AA;
 Query Match 92.6%; Score 2047.5; DB 4; Length 501;
 Best Local Similarity 80.4%; Pred. No. 2.6e-191;
 Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;
 QY 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLSACRNVLRRPFAQCCHRYCSFCLAS 60
 Db 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLSACRNVLRRPFAQCCHRYCSFCLAS 60
 QY 61 ILSGPNCAACVHEGIYEEGISESSAPPDPAARREVSLSFAVCPDCTCKWGLKE 120
 Db 61 ILSGPNCAACVHEGIYEEGISESSAPPDPAARREVSLSFAVCPDCTCKWGLKE 120
 QY 121 YE----- 122
 Db 121 YESCHEGRCPLMTECPACKGLVRLGKERHLEHECPERSLSRHRAPCCGADVKAHHE 180
 QY 123 -----FQDHVKTGCKRVPFCRPHAIGCLETVEGEKQOEHEVQWL 161
 Db 181 VCPKFPPLTCDGCGKKKIPREXFQDHVKTGCKRVPFCRPHAIGCLETVEGEKQOEHEVQWL 240
 QY 162 REHLAMLSSVLEAKPLLDQSHAGSELLOECSELEKKTATFENIVCVLNEVERVAMTA 221
 Db 241 REHLAMLSSVLEAKPLLDQSHAGSELLOECSELEKKTATFENIVCVLNEVERVAMTA 300
 QY 222 EACSRQHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKXVLEMEASTYDGVFIWKISD 281
 Db 301 EACSRQHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKXVLEMEASTYDGVFIWKISD 360
 QY 282 PARKLOEAVAGRIIPAISPAFTSRGYKMCRLRYLNGDGTGRTGTHLSLFFVNMKGPDA 341
 Db 361 ILRLQEAIVAGRIIPAISPAFTSRGYKMCRLRYLNGDGTGRTGTHLSLFFVNMKGPDA 420
 QY 342 LLRWPFNOKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDNMNIASGCPLFCFVSKNEA 401
 Db 421 LLRWPFNOKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDNMNIASGCPLFCFVSKNEA 480
 QY 402 KNSVVRDDAIFIKAIIVDLTGL 422
 Db 481 KNSVVRDDAIFIKAIIVDLTGL 501

RESULT 4
 ABO07170
 ID ABO07170 standard; protein; 501 AA.
 XX AC ABO07170;
 XX DT 13-AUG-2003 (first entry)
 XX DE Human p53 modifying protein, SEQ ID 130.
 XX KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KW apoptotic disorder; cell proliferation disorder.
 XX OS Homo sapiens.
 XX WO200229122-A1.
 XX PD 12-DEC-2002.
 XX PF 03-JUN-2002; 2002WO-US017382.
 XX PR 05-JUN-2001; 2001US-0296076P.
 XX PR 10-OCT-2001; 2001US-0328605P.
 XX PR 15-FEB-2002; 2002US-0357253P.

XX (EXEL-) EXELIXIS INC.
 XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 XX WPI; 2003-156859/15.
 XX N-PSDB; ACD13346.
 XX Identifying modulators of the p53 pathway for use in treating apoptotic
 XX or cell proliferation disorders, comprises screening for agents that
 XX modulate activity of a human ortholog of genes that modify the p53
 XX pathway in Drosophila.
 XX Example 2; Page 431-432; 678pp; English.
 XX The invention relates to identifying (M1) a candidate p53 pathway
 XX modulating agent, by contacting an assay system comprising a purified HM
 XX polypeptide (human orthologue of genes that modify the p53 pathway in
 XX Drosophila) or nucleic acid with a test agent under conditions, where but
 XX for the presence of the test agent, the system provides a reference
 XX activity, and detecting a test agent-biased activity of the assay system.
 XX Also included are modulating (M2) a p53 pathway of a cell (comprising
 XX contacting a cell defective in p53 function with a candidate modulator
 XX that specifically binds to a HM polypeptide comprising an HM amino acid
 XX sequence, where p53 function is restored), modulating (M3) a p53 pathway
 XX in a mammalian cell (comprising contacting the cell with an agent that
 XX specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
 XX a disease in a patient (comprising: (a) obtaining a biological sample
 XX from the patient; (b) contacting the sample with a probe for HM
 XX expression; (c) comparing the results with a control; and (d) determining
 XX whether the comparison indicates a likelihood disease). (M1) is useful
 XX for identifying modulators of the p53 pathway. A probe for HM expression
 XX is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
 XX in a patient, where the cancer has greater than 25 % expression level.
 XX Modulators identified by (M1) are useful in a variety of diagnostic and
 XX therapeutic applications, where disease or disorder prognosis is related
 XX to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 XX proliferation disorders (e.g. cancer). Another two new methods (M2 and
 XX M3) are useful for modulating the p53 pathway of a cell, thus restoring
 XX the p53 function of the cell, so that the cell undergoes normal
 XX proliferation or progression through the cell cycle. (M2) and (M3) are
 XX also useful for treating defects in the p53 pathway such as angiogenic,
 XX apoptotic or cell proliferation disorders. The present sequence
 XX represents a human p53 pathway modifying protein
 XX Sequence 501 AA;
 XX
 XX Query Match 92.6%; Score 2047.5; DB 6; Length 501;
 XX Best Local Similarity 80.4%; Pred. No. 2.6e-191;
 XX Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;
 QY 1 MAASVTPPGSLELLQPGFSTLLGTLKLEAKYLCACRNVLRRPFAQCCHRYCSFCLAS 60
 DB 1 MAASVTPPGSLELLQPGFSTLLGTLKLEAKYLCACRNVLRRPFAQCCHRYCSFCLAS 60
 QY 61 ILSSGPQNCACVHEGIVEEGISILESSAPDNNAREVESLPVCPDGCTWKGLKE 120
 DB 61 ILSSGPQNCACVHEGIVEEGISILESSAPDNNAREVESLPVCPDGCTWKGLKE 120
 QY 121 YE----- 122
 DB 121 YESCHEGRCPLMLTECPACKGLVRLGKERHLEHECPERSLSRCHRAPCCGADVAKAHE 180
 QY 123 -----FQHVTKGCRVPCPSHAIGCLVTEGKQHEVQWL 161
 DB 181 VCPFPLTDCGCKKIPREHFQHVTKGCRVPCPSHAIGCLVTEGKQHEVQWL 240
 QY 162 REHLAMLSSVLEAKPLLDQSHAGSELQRCESLEKKTATFENIVCVLNERERVANTA 221
 DB 241 REHLAMLSSVLEAKPLLDQSHAGSELQRCESLEKKTATFENIVCVLNERERVANTA 300
 QY 222 EACSRHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKVRPFAQCCHRYCSFCLAS 281
 DB 281 EACSRHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKVRPFAQCCHRYCSFCLAS 360

DB 301 EACSRHRLDQDKIEALSSKVQQLERSIGLKDLAMADLEQKVRPFAQCCHRYCSFCLAS 360
 QY 282 PARKLOEAVAGHAIPIAFSPAFYTSRYGYKMCILRIYVINGGTCGRGTHLSLFFVWVKGRNDA 341
 DB 361 ILRLKOEAVAGHAIPIAFSPAFYTSRYGYKMCILRIYVINGGTCGRGTHLSLFFVWVKGRNDA 420
 QY 342 LLRWPFNQKVTLMMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIIASCPLFCFVSKMEA 401
 DB 421 LLRWPFNQKVTLMMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIIASCPLFCFVSKMEA 480
 QY 402 KNSYVRDDAIFKAIKIVDLTGL 422
 DB 481 KNSYVRDDAIFKAIKIVDLTGL 501
 XX
 XX RESULT 5
 XX ADB80956
 XX ID ADB80956 standard; protein; 501 AA.
 XX AC ADB80956;
 XX DT 04-DEC-2003 (first entry)
 XX DE RING-SH complex related protein, SEQ ID No 30.
 XX KW RING-SH 3; Gag protein; Gag late domain; P13K; actin; myosin; Hsp60;
 XX Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; tsg101;
 XX cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
 XX rhabdovirus; filovirus.
 XX OS Unidentified.
 XX PN WO2003033646-A2.
 XX PD 24-APR-2003.
 XX PF 31-JUL-2002; 2002WO-US024589.
 XX PR 31-JUL-2001; 2001US-0308958P.
 XX PR 09-NOV-2001; 2001US-0345846P.
 XX PA (PROT-) PROTEOLOGICS INC.
 XX PI Greener T, Moskowitz H, Reiss Y, Alroy I;
 XX WPI; 2003-393509/37.
 XX N-PSDB; ADB80997.
 XX New isolated protein complex comprising a RING-SH 3 polypeptide and
 XX another polypeptide, useful for detecting cells infected with a virus,
 XX and for treating viral disorders caused by retroviruses, rhabdoviruses,
 XX or filoviruses.
 XX Disclosure; Fig 30; 176pp; English.
 XX The invention relates to a novel isolated protein complex comprising a
 XX RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
 XX Gag late domain, P13K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A,
 XX STAM2B, VHS-UIM, a GTPase, an E2 enzyme, tsg101, a cullin, RING-SH, and a
 XX clathrin. The novel protein complex has virucide activity and can be used
 XX to treat disorders as part of a vaccine. The protein complex and
 XX composition are useful for detecting cells infected with a virus, for
 XX identifying agents having antiviral activity, and for treating viral
 XX disorders caused by retroviruses, rhabdoviruses, or filoviruses. This
 XX sequence is a protein comprising the RING-SH complex of the invention.
 XX Sequence 501 AA;
 XX
 XX Query Match 92.6%; Score 2047.5; DB 7; Length 501;
 XX Best Local Similarity 80.4%; Pred. No. 2.6e-191;
 XX Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;
 QY 1 MAASVTPPGSLELLQPGFSTLLGTLKLEAKYLCACRNVLRRPFAQCCHRYCSFCLAS 60

```

Db      1 MAAASVTPPGSLELLQPGFSKTLTGKLEAKYLCSACRNVLRRPFOACGHRVCSFCLAS 60
QY      61 ILSSGPQNCACVHEGIIYEGISILESSAFPNDNAARREVESLPVCPSDGCTWKGTIKE 120
Db      61 ILSSGPQNCACVHEGIIYEGISILESSAFPNDNAARREVESLPVCPSDGCTWKGTIKE 120
QY      121 YE----- 122
Db      121 YSCHGRCPLMLTECPACKGLVRLGKERHLEHCEPERSLSRCHRAPCCGADVKAHHE 180
QY      123 -----FQDHVKTGCKRVPFCRFRHAIGCLTVEGKQOEHEVQWL 161
Db      181 VCPKPLTCDGGCKKIPREKFQDHVKTGCKRVPFCRFRHAIGCLTVEGKQOEHEVQWL 240
QY      162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221
Db      241 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 300
QY      222 EACSRQRLDQDKIEALSKVQQLERSIGLKDLAMADLEQKYLEMASTYDGVFIWKISD 281
Db      301 EACSRQRLDQDKIEALSKVQQLERSIGLKDLAMADLEQKYLEMASTYDGVFIWKISD 360
QY      282 PARKLOEAVAGRIPAFSPAFYTSRYGYKWCILRIYLNQDGTGRGTHLSLFFVVMKGPND 341
Db      341 ILRLQOEAVAGRIPAFSPAFYTSRYGYKWCILRIYLNQDGTGRGTHLSLFFVVMKGPND 420
QY      342 LLRWPFNQKVTMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNTASGCPFCPVSKMEA 401
Db      421 LLRWPFNQKVTMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNTASGCPFCPVSKMEA 480
QY      402 KNSYVRDDAIFKAIVDLTGL 422
Db      481 KNSYVRDDAIFKAIVDLTGL 501

RESULT 6
ABR84599
ID ABR84599 standard; protein; 501 AA.
AC
XX
AC ABR84599;
XX
DT 18-DEC-2003 (first entry)
DE
DE TRAF2 protein.
XX
KW TRAF2; inflammatory response; rheumatoid arthritis; LtbetaR;
KW lymphotoxin-beta receptor; modulator; cancer; immunological disease;
KW apoptosis; cytostatic; immunosuppressive; antirheumatic; antiarthritic;
KW antiinflammatory; dermatological; nephrotropic; antithyroid;
KW thymineimetic; muscular-Gen; neuroprotective; antianaemic; haemostatic;
KW vasotropic; antidiabetic.
XX
OS Unidentified.
XX
XX WO2003066834-A2.
XX
XX 14-AUG-2003.
XX
XX 10-FEB-2003; 2003WO-US003923.
XX
XX 08-FEB-2002; 2002US-0355183P.
XX
XX (AMVP ) WYETH.
XX
XX Kuai J, Wooters JL, Nickbarg EB, Qiu Y, Lin L;
XX
XX WPI; 2003-748125/70.
XX
XX N-PSDB; ACF04633.
XX
XX New purified lymphotoxin-beta receptor protein complex, useful for
XX identifying modulators of lymphotoxin-beta receptor activity or
XX expression for treating or preventing cancer or an autoimmune disorder,

```

```

PT      e.g. vasculitis or diabetes.
XX
XX Disclosure; Page 6; Opp; English.
XX
CC The present invention relates to a purified complex comprising a
CC lymphotoxin beta receptor (LtbetaR) polypeptide and Smac polypeptide. The
CC lymphotoxin-beta receptor (LtbetaR) complex is useful for identifying
CC modulators of LtbetaR activity or expression for treating or preventing
CC cancer or an immune disorder such as autoimmune disorder, e.g. rheumatoid
CC arthritis, systemic lupus erythematosus, Goodpasture's syndrome, Grave's
CC disease, Hashimoto's thyroiditis, pemphigus vulgaris, myasthenia gravis,
CC scleroderma, autoimmune haemolytic anaemia, autoimmune thrombocytopenic
CC purpura, polymyositis, dermatomyositis, pernicious anaemia, Sjogren's
CC syndrome, ankylosing spondylitis, vasculitis, or type I diabetes
CC mellitus. The present sequence is a TRAF2 protein, which forms part of
CC the complex of the invention
XX
XX Sequence 501 AA;

Query Match      92.6%; Score 2047.5; DB 7; Length 501;
Best Local Similarity 80.4%; Pred. No. 2.6e-191;
Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;

QY      1 MAAASVTPPGSLELLQPGFSKTLTGKLEAKYLCSACRNVLRRPFOACGHRVCSFCLAS 60
Db      1 MAAASVTPPGSLELLQPGFSKTLTGKLEAKYLCSACRNVLRRPFOACGHRVCSFCLAS 60
QY      61 ILSSGPQNCACVHEGIIYEGISILESSAFPNDNAARREVESLPVCPSDGCTWKGTIKE 120
Db      61 ILSSGPQNCACVHEGIIYEGISILESSAFPNDNAARREVESLPVCPSDGCTWKGTIKE 120
QY      121 YE----- 122
Db      121 YESCHGRCPLMLTECPACKGLVRLGKERHLEHCEPERSLSRCHRAPCCGADVKAHHE 180
QY      123 -----FQDHVKTGCKRVPFCRFRHAIGCLTVEGKQOEHEVQWL 161
Db      181 VCPKPLTCDGGCKKIPREKFQDHVKTGCKRVPFCRFRHAIGCLTVEGKQOEHEVQWL 240
QY      162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221
Db      241 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 300
QY      222 EACSRQRLDQDKIEALSKVQQLERSIGLKDLAMADLEQKYLEMASTYDGVFIWKISD 281
Db      301 EACSRQRLDQDKIEALSKVQQLERSIGLKDLAMADLEQKYLEMASTYDGVFIWKISD 360
QY      282 PARKLOEAVAGRIPAFSPAFYTSRYGYKWCILRIYLNQDGTGRGTHLSLFFVVMKGPND 341
Db      341 ILRLQOEAVAGRIPAFSPAFYTSRYGYKWCILRIYLNQDGTGRGTHLSLFFVVMKGPND 420
QY      342 LLRWPFNQKVTMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNTASGCPFCPVSKMEA 401
Db      421 LLRWPFNQKVTMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNTASGCPFCPVSKMEA 480
QY      402 KNSYVRDDAIFKAIVDLTGL 422
Db      481 KNSYVRDDAIFKAIVDLTGL 501

RESULT 7
ADM45822
ID ADM45822 standard; protein; 501 AA.
XX
AC ADM45822;
XX
XX 03-JUN-2004 (first entry)
XX
XX TNF-alpha receptor complex-related TRAF2 protein.
XX
XX protein complex; tumour necrosis factor alpha receptor; TNF-alpha; TNFR;
XX nuclear factor; NF-kappaB activating kinase; NAK; RasGAP3;
XX transducin repeat-containing protein; TRCP1; TRCP2; antiinflammatory;

```



```

Db      121 YESCHEGLCPFLTECPACKGLVRLSEKHEHTEQCPKRSLSQCHCAPSHVDLVHYE 180
QY      123 -----FQDHVKTGCKRVPCHFAIGCLETVEGEKQOEHEVQWL 161
Db      181 VCPKPLTCDGCGKKXIPRETQDQHVACSKRVLRFHTVGCSEMVETENLQDHELQRL 240
QY      162 REHLAMLSSVLEAKPLLDQSHAGSELLORCESLEKKTATFENIVCVLNREVERVAMTA 221
Db      241 REHLALLSFLAQSPGTLNQVGPPELLQRCILEQKTIATFENIVCVLNREVERVAMTA 300
QY      222 EACSRQRLDQDKIEALSCKVQQLERSIGLKDAMADLEQKYLEMEASTYDGVFWKISD 281
Db      301 EACSRQRLDQDKIEALSCKVQQLERSIGLKDAMADLEQKYLEMEASTYDGVFWKISD 360
QY      282 PARKLOEAVAGRIPAIFSPAFYTSRYGYKMLRIYINGDGTGRGTHLSLFFVVMKGNDA 341
Db      361 FTRKQEAAGRTPAIFSPAFYTSRYGYKMLRIYINGDGTGRGTHLSLFFVVMKGNDA 420
QY      342 LLRWPFNQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVDMNTASGCPLEFCPVSKMEA 401
Db      421 LLQWPFNQKVTMLLDHNNREHVIDAFRDPDVTSSSFQRPVDMNTASGCPLEFCPVSKMEA 480
QY      402 KNSYVRDDAIFKAIVDLTGL 422
Db      481 KNSYVRDDAIFKAIVDLTGL 501

RESULT 9
ID AAR90578 standard; protein; 501 AA.
XX
AC AAR90578;
DT 09-APR-1996 (first entry)
DE Mouse TRAF2.
XX
KW TRAF2; tumour necrosis factor receptor associated factor 2; TNF; CD40.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Domain 272..501
FT Region 275..351
FT /label= TRAF_domain
FT /label= Leucine_zipper_region
XX
PN WO9533051-A1.
XX
PD 07-DEC-1995.
XX
PF 25-MAY-1995; 95WO-US0006639.
XX
PR 27-MAY-1994; 94US-00250858.
PR 28-OCT-1994; 94US-00331394.
PR 22-MAY-1995; 95US-00446915.
XX
PA (GETH ) GENENTECH INC.
XX
XX Goeddel DV, Rothe M;
XX
XX WPI; 1996-049310/05.
DR N-PSDB; AAT12262.
XX
XX Tumour necrosis factor (TNF) receptor-associated factors - involved in
PT mediation of biological activities of TNF and CD40 ligands.
XX
XX Claim 8; Page 75-76; 116pp; English.
XX
XX Mouse tumour necrosis factor receptor associated factor 2 (TRAF2)
CC (AAR90578) is a new factor capable of specific association with the
CC intracellular domain of the type 2 TNF receptor (TNF-R2) and CD40, and is
```

```

CC involved in the mediation of TNF and CD40 ligand biological activities.
CC Recombinant TRAF2 is obt'd. by expression in host cells of a cDNA clone
CC (AAR12262) isolated using a yeast two-hybrid assay. It is used to
CC identify inhibitors of activities of TNF-R2, CD40 and/or LMP1 oncogene,
CC e.g. for treatment of endotoxic (septic) shock and rheumatoid arthritis
XX
XX Sequence 501 AA;
QY
Query Match 86.4%; Score 1909.5; DB 2; Length 501;
Best Local Similarity 74.1%; Pred. No. 8.8e-178;
Matches 371; Conservative 22; Mismatches 29; Indels 79; Gaps 1;
QY 1 MAASVTPPGSLELLQPGFSKTLIGTLEAKYLCSACRNVLRRPFOACQGHRYSCFLAS 60
Db 1 MAASVTPSPGSELLQPGFSKTLIGTLEAKYLCSACKNLLRRPFOACQGHRYSCFLTS 60
QY 61 ILSSGPONCAACVHEGYIEGISESSAPFPDPAARREVESIPAVCPDGCCTWKGLTKE 120
Db 61 ILSSGPQDCAACVGYEGLYEGISESSAPFPDPAARREVESIPAVCPDGCCTWKGLTKE 120
QY 121 YE----- 122
Db 121 YESCHEGLCPFLTECPACKGLVRLSEKHEHTEQCPKRSLSQCHCAPSHVDLVHYE 180
QY 123 -----FQDHVKTGCKRVPCHFAIGCLETVEGEKQOEHEVQWL 161
Db 181 VCPKPLTCDGCGKKXIPRETQDQHVACSKRVLRFHTVGCSEMVETENLQDHELQRL 240
QY 162 REHLAMLSSVLEAKPLLDQSHAGSELLORCESLEKKTATFENIVCVLNREVERVAMTA 221
Db 241 REHLALLSFLAQSPGTLNQVGPPELLQRCILEQKTIATFENIVCVLNREVERVAMTA 300
QY 222 EACSRQRLDQDKIEALSCKVQQLERSIGLKDAMADLEQKYLEMEASTYDGVFWKISD 281
Db 301 EACSRQRLDQDKIEALSCKVQQLERSIGLKDAMADLEQKYLEMEASTYDGVFWKISD 360
QY 282 PARKLOEAVAGRIPAIFSPAFYTSRYGYKMLRIYINGDGTGRGTHLSLFFVVMKGNDA 341
Db 361 FTRKQEAAGRTPAIFSPAFYTSRYGYKMLRIYINGDGTGRGTHLSLFFVVMKGNDA 420
QY 342 LLRWPFNQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVDMNTASGCPLEFCPVSKMEA 401
Db 421 LLQWPFNQKVTMLLDHNNREHVIDAFRDPDVTSSSFQRPVDMNTASGCPLEFCPVSKMEA 480
QY 402 KNSYVRDDAIFKAIVDLTGL 422
Db 481 KNSYVRDDAIFKAIVDLTGL 501

RESULT 10
ID AAY71902
XX AAY71902 standard; protein; 336 AA.
AC AAY71902;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human TRAF2TR variant, TRAF2 truncated-deleted (TRAF2TD) protein.
XX
KW Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
KW TNF-receptor associated factor; TRAF2 truncated-deleted; TRAF2TD;
KW antiinflammatory; cardiant; mutant; mutein; myocardial infarction;
KW vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
KW antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;
KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
KW neurodegenerative disease; variant; TRAF2 truncated; TRAF2TR.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO2000066737-A1.
XX
```

PD 09-NOV-2000.
 XX
 PF 06-APR-2000; 2000WO-US009178.
 XX
 PR 30-APR-1999; 99US-0131940P.
 XX
 PA (AVET) AVENTIS PHARM PROD INC.
 XX
 XX Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
 XX WPI; 2001-007223/01.
 DR N-PSDB; AAD01948.
 XX
 XX New nucleic acid encoding variants of tumor necrosis factor receptor
 PT associated factors useful for inhibiting tumor necrosis factor alpha-
 PT regulated pathways, and for treating Crohn's disease, psoriasis, and
 PT rheumatoid arthritis.
 XX
 XX Claim 6; Fig 3b; 74pp; English.
 PS
 XX The present sequence is tumor necrosis factor (TNF)-receptor associated
 CC factor truncated-deleted (TRAP2TD) protein. This sequence includes the
 CC naturally occurring splice variation and a deletion at the N-terminal end
 CC of human TRAF2 protein. The TRAF2D variant is useful for inhibiting
 CC diseases involving over production of TNFalpha, TNFalpha pathologies
 CC involving hyperactivation of nuclear factor kappa B (NFkB). The variant
 CC is also useful for inhibiting and treating inflammatory processes
 CC involving TNFalpha such as Crohn's disease, psoriasis, rheumatoid
 CC arthritis, graft versus host disease, non-insulin dependent diabetes,
 CC inflammatory bowel disease, and neurodegenerative diseases or
 CC cardiovascular disease such as cardiac ischaemia-reperfusion injury
 CC following myocardial infarction, coronary artery bypass surgery, cardiac
 CC transplantation or ischaemia-reperfusion injury in the central nervous
 CC system (CNS) following stroke, the progression and rupture of advanced
 CC coronary atherosclerotic plaques, development and progression of
 CC congestive heart failure, endothelial cell injury following balloon
 CC angioplasty, or apoptotic cell death of myocardial cells
 XX
 SQ Sequence 336 AA;
 Query Match 79.2%; Score 1751; DB 4; Length 336;
 Best Local Similarity 100.0%; Pred. No. 1.7e-162;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 88 SSAPPDNAAREVESLPAVCPDSDGCTWGTUKEVEFDQHVKTCKRVPFCRFAIGCLET 147
 DB 2 SSAPPDNAAREVESLPAVCPDSDGCTWGTUKEVEFDQHVKTCKRVPFCRFAIGCLET 61
 QY 148 VEGEKQOEHEVQWLRHLAMLLSSVLEAKPLGQSHAGSELLQRCSELEKKTATFNIV 207
 DB 62 VEGEKQOEHEVQWLRHLAMLLSSVLEAKPLGQSHAGSELLQRCSELEKKTATFNIV 121
 QY 208 CVLAREVERVANTAEACSRQRLDQDKIEALSSKVVQLERSIGLKDLAMADLEQKYLEME 267
 DB 122 CVLAREVERVANTAEACSRQRLDQDKIEALSSKVVQLERSIGLKDLAMADLEQKYLEME 181
 QY 268 ASTVDGVFIWKISDFARKLQAVAGRIPALFSPAFYTSRYGKNCRLIYINGDGTGRGTH 327
 DB 182 ASTVDGVFIWKISDFARKLQAVAGRIPALFSPAFYTSRYGKNCRLIYINGDGTGRGTH 241
 QY 328 LSLFFVVMKGNPDALLRWFNFQKVTLLDQNNREHVIDAFRDPVTSSTSSFRPVDNMNIA 387
 DB 242 LSLFFVVMKGNPDALLRWFNFQKVTLLDQNNREHVIDAFRDPVTSSTSSFRPVDNMNIA 301
 QY 388 SGCPLFCPSVSKMEAKNSVYRDDAIFIKAVDLTGL 422
 DB 302 SGCPLFCPSVSKMEAKNSVYRDDAIFIKAVDLTGL 336
 RESULT 11
 ID ADA54134 standard; protein; 447 AA.
 XX

AC ADA54134;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human protein, SEQ ID 1702.
 XX
 XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX
 XX Homo sapiens.
 OS
 XX EP1293569-A2.
 PN
 XX 19-MAR-2003.
 PD
 XX 21-MAR-2002; 2002EP-00006586.
 PF
 XX 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 PR
 XX (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Izie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX WPI; 2003-395639/38.
 DR N-PSDB; ADA52495.
 DR
 XX New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX
 XX Claim 14; SEQ ID NO 1702; 205pp; English.
 XX
 XX The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.
 CC
 SQ Sequence 447 AA;
 Query Match 73.8%; Score 1631.5; DB 6; Length 447;
 Best Local Similarity 73.6%; Pred. No. 1.3e-150;
 Matches 340; Conservative 17; Mismatches 50; Indels 55; Gaps 9;
 QY 1 YAAASVTPGSLLELQPGFSKTLTGKLEAKYLCACRNVLRRPQACGHRYSFCFLAS 60
 DB 1 YAAASVTPGSLLELQPGFSKTLTGKLEAKYLCACRNVLRRPQACGHRYSFCFLAS 60
 QY 61 ILSGSPQCAACVHSGIYEEGSIILESSAPDPAAREVESLPAVCPDSDGCTWGTILKE 120
 DB 61 ILSGSPQCAACVHSGIYEEGSIILESSAPDPAAREVESLPAVCPDSDGCTWGTILKE 120
 QY 121 YEFQDHVKTG-----KCRVPCRFAI-----GCLETVEGEKQOEHEVQWL 161
 DB 121 YEVK--MPACGMVTAPAVGSRPRSPSYDLVLHVLVTGAECALMSVEETE----- 170
 QY 162 REHLAMLLSSVLEAK-PL-----LGD-QSHAGSELLQRCSELEKKTATFNIV 206
 DB 171 -----LLRSCHGRCPLMLTECPACKGLVRLGEKHEHLECPERSLSRCHCAPCCGA 225
 QY 207 VCVLNREV-ERVAMTAEACS-----RQRLDQDKIEALSSKVVQLERSIGLKDLAMADLE 260
 DB 226 DVKAHHEVCPRPPLTCDGCGKKKIPREKFDQDKIEALSSKVVQLERSIGLKDLAMADLE 285
 QY 261 OKVLEMEASTVDGVFIWKISDFARKLQAVAGRIPALFSPAFYTSRYGKNCRLIYINGD 320
 DB 286 QKVLEMEASTVDGVFIWKISDFARKLQAVAGRIPALFSPAFYTSRYGKNCRLIYINGD 345

```
QY 321 GTGGRGTHLSLFFVVMKGNDAILLRWFNOKVTLMLLDQNNRHHVIDAREPDTVTSSSFQRP 380
DB 346 GTGGRGTHLSLFFVVMKGNDAILLRWFNOKVTLMLLDQNNRHHVIDAREPDTVTSSSFQRP 405
QY 381 VNDMNTASGCLPCPVSKMEAKNSYVRDDAIFKAIVDLTGL 422
DB 406 VNDMNTASGCLPCPVSKMEAKNSYVRDDAIFKAIVDLTGL 447

RESULT 12
AAB07002
ID AAB07002 standard; protein; 243 AA.
XX AC
XX AAB07002;
XX DT
XX 17-OCT-2000 (first entry)
XX DE
XX Human TRAF2(NC)-CA21 protein.
XX KW
XX Human; TRAF(NC)-CA21 protein; Tumour-necrosis factor; TNF;
XX TNF receptor-associated factor; cell proliferation; cell differentiation;
XX apoptosis; inflammation; immune response; receptor-ligand binding assay.
XX OS
XX Homo sapiens.
XX FN
XX WO200026670-A1.
XX PD
XX 11-MAY-2000.
XX PF
XX 23-AUG-1999; 99WO-US019272.
XX PR
XX 29-OCT-1998; 98US-00181958.
XX PA
XX (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX PI
XX Kehry MR, Pullen SS, Crute JJ;
XX XX
DR WPI; 2000-451628/39.
XX PT
XX Quantitative assay for measuring the effect of a substance on tumor
XX necrosis factor receptor associated factor protein interaction with it
XX receptor.
XX PS
XX Claim 7; Page 19-21; 27pp; English.
XX CC
XX Tumour necrosis factor (TNF) receptor has an important role in the
XX regulation of cellular proliferation, differentiation, and apoptosis in
XX inflammatory and immune responses. The present invention relates to a
XX quantitative assay for measuring the ability of a substance to effect
XX binding of a TNF receptor-associated factor (TRAF) protein to its
XX receptor. The present sequence is Human TRAF(NC)-CA21 protein fragment,
XX which was used in the present assay. This protein is the conserved C-
XX terminal region (NC) of TRAF2, and possesses a C-terminal tag that is
XX recognised by CA21 monoclonal antibody. Proteins which bind to the
XX present sequence are detected by CA21 antibody which generates a signal
XX
XX Sequence 243 AA;

Query Match 53.3%; Score 1178; DB 3; Length 243;
Best Local Similarity 99.6%; Pred. No. 1.5e-106;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CESLEKKTATFENIVCVLNEVERVAMTAACSRQHRLLDQDKTEALSKVQQLERSIGLK 252
DB 1 CESLEKKTATFENIVCVLNEVERVAMTAACSRQHRLLDQDKTEALSKVQQLERSIGLK 60
QY 253 DLAMADLEQKVLMEASTVDGVFIWKISDFARKLQEAAGRIAPAFSPAFYTSRYGYKVC 312
DB 61 DLAMADLEQKVLMEASTVDGVFIWKISDFARKLQEAAGRIAPAFSPAFYTSRYGYKVC 120
QY 313 LRIYLNGDGTGRGTHLSLFFVVMKGNDAILLRWFNOKVTLMLLDQNNRHHVIDAREPDTV 372
DB 121 LRIYLNGDGTGRGTHLSLFFVVMKGNDAILLRWFNOKVTLMLLDQNNRHHVIDAREPDTV 180
```

```
QY 373 TSSSFQRPVNDMNTASGCLPCPVSKMEAKNSYVRDDAIFKAIVDLTGL 422
DB 181 TSSSFQRPVNDMNTASGCLPCPVSKMEAKNSYVRDDAIFKAIVDLTGL 230

RESULT 13
AUB07084
ID AUB07084 standard; protein; 326 AA.
XX AC
XX AUB07084;
XX DT
XX 10-JUN-2003 (first entry)
XX DE
XX Human adipocyte Selected Interacting domain, SID, #415.
XX KW
XX Human; prey; adipocyte; SID; selected interacting domain; anorectic;
XX antidiabetic; protein-protein interaction; diabetes;
XX yeast 2-hybrid assay; metabolic disorder; obesity.
XX OS
XX Homo sapiens.
XX FN
XX WO2000286122-A2.
XX PD
XX 31-OCT-2002.
XX PF
XX 14-MAR-2002; 2002WO-EP003768.
XX PR
XX 14-MAR-2001; 2001US-0275734P.
XX PA
XX (HYBR-) HYBRIGENICS.
XX PI
XX Legrain P, Daviet L;
XX DR
XX WPI; 2003-103412/09.
XX DR
XX N-PSDB; ACAS7328.
XX PT
XX New complex between two interacting proteins in adipocyte cells, useful
XX for identifying selected interacting domains that modulate protein
XX interactions, or for preventing or treating metabolic disorders such as
XX obesity or diabetes.
XX PS
XX Claim 6; Page 249; 382pp; English.
XX CC
XX The invention relates to a complex between two interacting proteins in
XX adipocyte cells, given in the specification. The proteins are identified
XX by selecting a bait protein from a known adipocyte marker and then
XX performing a yeast 2-hybrid selection to isolate prey proteins encoded by
XX members of an adipocyte cDNA library. The proteins are designated SID
XX (RTM) (selected interacting domains) proteins. Also included are a
XX polynucleotide encoding a polypeptide in the adipocyte cells, a
XX recombinant host cell expressing at least one of the interacting
XX polypeptides of the complex, selecting a modulating compound in adipocyte
XX cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
XX sequences given in the specification (including its fragment or variant),
XX a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
XX given in the specification (including its fragment or variant), a vector
XX comprising the SID (RTM) polynucleotide, a recombinant host cell
XX comprising the vector, a protein chip comprising the polypeptides and a
XX record comprising all or part of the data, listed in the specification.
XX The complex, polypeptides, polynucleotides and compounds are useful for
XX preventing or treating metabolic disorders such as obesity or diabetes.
XX The polynucleotides are useful as probes or primers. The complex is
XX particularly useful for identifying selected interacting domains (SID
XX (RTM)) for screening drugs that modulate the protein interaction, thus
XX exhibiting the therapeutic effect. The present sequence represents a SID
XX (prey) protein of the invention
XX
XX Sequence 326 AA;
```

Query Match 45.2%; Score 999.5; DB 6; Length 326;
Best Local Similarity 67.8%; Pred. No. 7.6e-89;
Matches 219; Conservative 13; Mismatches 48; Indels 43; Gaps 7;

This Page Blank (uspto)

Db 1 MAASVTSPGSLLELQPGFSKTLTGRLLEAKYLSACKNILLRRPFAQCCHRYCSFCLTS 60
Qy 61 ILSSGPQCAACVHEGIEGSILESSAPPDNNARREVESLPVCPDGTWKGTLKE 120
Db 61 ILSSGPQCAACVHEGIEGSILESSAPPDNNARREVESLPVCPDGTWKGTLKE 120
Qy 121 YE----- 122
Db 121 YESCHEGLCPFLTECPACKGLVRLSEKEHTEOECPKRSLSQCHRAPCSHVDLEVHYE 180
Qy 123 -----FQDHVTCGKCRVPCRFHAIGCLTVEGEKQHEVQWL 161
Db 181 VCPKFLTCDCGCKKKIPRETFOHVRACSKRVLCRFHTVGCSEMVETENLQDHELQRL 240
Qy 162 REHLAMLLSSVLEAKPLLDGSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAVTA 221
Db 241 REHLALLSSLEAQAASPTLNQVGPPELLQRCQILEQKIATFENIVCVLNREVERVAVTA 300
Qy 222 EACSRQHLDDQKTEALSSKVQQLERSIGLXDLAMADLEQKVLEMEASTYDGVFIWKISD 281
Db 301 EACSRQHLDDQKTEALSSKVQQLERSIGLXDLAMADLEQKVSELEVSTYDGVFIWKISD 360
Qy 282 FARLQEAAGRIIPAISPAFYTSRYGYKMLRYLNGDGTGRGTHLSLFFVVMKGNDA 420
Db 361 FTRKQEAAGRTPAISPAFYTSRYGYKMLRYLNGDGTGRGTHLSLFFVVMKGNDA 420
Qy 342 LLRWPFNQKVTMLLDQNNREHVIDAFRDPVTSFSSFORPVNDMMNIASGCLPFCPVSKMEA 401
Db 421 LLQWPFNOKVTMLLDHNNREHVIDAFRDPVTSFSSFORPVSDMMNIASGCLPFCPVSKMEA 480
Qy 402 KNSYVRDDAIFKAIVDLTGL 422
Db 481 KNSYVRDDAIFKAIVDLTGL 501

RESULT 2

US-08-250-858-4
; Sequence 4, Application US/08250858
; Patent No. 5708142
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,858
; FILING DATE: 27-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,065
; REFERENCE/DOCKET NUMBER: 897.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-250-858-4
Query Match 86.6%; Score 1914.5; DB 1; Length 501;
Best Local Similarity 74.3%; Pred. No. 6.4e-184;
Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

Qy 1 MAASVTSPGSLLELQPGFSKTLTGRLLEAKYLSACKNILLRRPFAQCCHRYCSFCLAS 60
Db 1 MAASVTSPGSLLELQPGFSKTLTGRLLEAKYLSACKNILLRRPFAQCCHRYCSFCLTS 60
Qy 61 ILSSGPQCAACVHEGIEGSILESSAPPDNNARREVESLPVCPDGTWKGTLKE 120
Db 61 ILSSGPQCAACVHEGIEGSILESSAPPDNNARREVESLPVCPDGTWKGTLKE 120
Qy 121 YE----- 122
Db 121 YESCHEGLCPFLTECPACKGLVRLSEKEHTEOECPKRSLSQCHRAPCSHVDLEVHYE 180
Qy 123 -----FQDHVTCGKCRVPCRFHAIGCLTVEGEKQHEVQWL 161
Db 181 VCPKFLTCDCGCKKKIPRETFOHVRACSKRVLCRFHTVGCSEMVETENLQDHELQRL 240
Qy 162 REHLAMLLSSVLEAKPLLDGSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAVTA 221
Db 241 REHLALLSSLEAQAASPTLNQVGPPELLQRCQILEQKIATFENIVCVLNREVERVAVTA 300
Qy 222 EACSRQHLDDQKTEALSSKVQQLERSIGLXDLAMADLEQKVLEMEASTYDGVFIWKISD 281
Db 301 EACSRQHLDDQKTEALSSKVQQLERSIGLXDLAMADLEQKVSELEVSTYDGVFIWKISD 360
Qy 282 FARLQEAAGRIIPAISPAFYTSRYGYKMLRYLNGDGTGRGTHLSLFFVVMKGNDA 420
Db 361 FTRKQEAAGRTPAISPAFYTSRYGYKMLRYLNGDGTGRGTHLSLFFVVMKGNDA 420
Qy 342 LLRWPFNQKVTMLLDQNNREHVIDAFRDPVTSFSSFORPVNDMMNIASGCLPFCPVSKMEA 401
Db 421 LLQWPFNOKVTMLLDHNNREHVIDAFRDPVTSFSSFORPVSDMMNIASGCLPFCPVSKMEA 480
Qy 402 KNSYVRDDAIFKAIVDLTGL 422
Db 481 KNSYVRDDAIFKAIVDLTGL 501

RESULT 3

US-08-446-915-4
; Sequence 4, Application US/08446915
; Patent No. 5741667
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,915
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858

FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA: 08/331394
APPLICATION NUMBER: 08/331394
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897P2
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-446-915-4

Query Match 86.6%; Score 1914.5; DB 1; Length 501;
Best Local Similarity 74.3%; Pred. No. 6.4e-184;
Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAAASVTPGSLLELQPGSKLLGTLKLEAKYLCACRNVLRRPFAQCQGHRYCSFCLAS 60
DB 1 MAAASVTPGSLLELQPGSKLLGTLKLEAKYLCACRNVLRRPFAQCQGHRYCSFCLTS 60
QY 61 ILSSGPONCAACVHEGYEGISILESSAFPDNAARREVESLPVCFSDGCTWKGTLKE 120
DB 61 ILSSGPONCAACVHEGYEGISILESSAFPDNAARREVESLPVCFNDGCTWKGTLKE 120
QY 121 YE----- 122
DB 121 YESCHEGLCPFLITECPACKGLVRLSEKHEHTEQECPKESLSQCQCRAPCSHVDLEVHYE 180
QY 123 -----FQDHVKTGCKRVPCEFAIGCLETVGEKQOEHEVOWL 161
DB 181 VCPKPLTCDGCGKKIPRETQDQHVACSKRVLCTFHTVGCSEMVETENLQDHELQRL 240
QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCSELEKKTATFENIVCLNREVERVAMTA 221
DB 241 REHLALLSSFLAEQAQSPGLNQVGPPELLQRCQLEQKIATFENIVCLNREVERVAVTA 300
QY 222 EACSRQHRLDQDKIEALSCKVQQLERSIGLKDLAMADLEQKLEMEASTYDGVFIWKISD 281
DB 301 EACSRQHRLDQDKIEALSCKVQQLERSIGLKDLAMADLEQKLEMEASTYDGVFIWKISD 360
QY 342 LLRWPNQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVDMNTIASGCPFCFVSKMEA 401
DB 421 LLQWPFNQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVDMNTIASGCPFCFVSKMEA 480
QY 402 KNSYVRDDAIFKAIIVDLTGL 422
DB 481 KNSYVRDDAIFKAIIVDLTGL 501

RESULT 4
US-08-744-139-4
Sequence 4, Application US/08744139
Patent No. 5863612
GENERAL INFORMATION:
APPLICANT: Goeddel, David V
APPLICANT: Rothe, Mike
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,139
FILING DATE: 31-Oct-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250858
FILING DATE: 05/27/1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P0897C1
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-744-139-4

Query Match 86.6%; Score 1914.5; DB 2; Length 501;
Best Local Similarity 74.3%; Pred. No. 6.4e-184;
Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAAASVTPGSLLELQPGSKLLGTLKLEAKYLCACRNVLRRPFAQCQGHRYCSFCLAS 60
DB 1 MAAASVTPGSLLELQPGSKLLGTLKLEAKYLCACRNVLRRPFAQCQGHRYCSFCLTS 60
QY 61 ILSSGPONCAACVHEGYEGISILESSAFPDNAARREVESLPVCFSDGCTWKGTLKE 120
DB 61 ILSSGPONCAACVHEGYEGISILESSAFPDNAARREVESLPVCFNDGCTWKGTLKE 120
QY 121 YE----- 122
DB 121 YESCHEGLCPFLITECPACKGLVRLSEKHEHTEQECPKESLSQCQCRAPCSHVDLEVHYE 180
QY 123 -----FQDHVKTGCKRVPCEFAIGCLETVGEKQOEHEVOWL 161
DB 181 VCPKPLTCDGCGKKIPRETQDQHVACSKRVLCTFHTVGCSEMVETENLQDHELQRL 240
QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCSELEKKTATFENIVCLNREVERVAMTA 221
DB 241 REHLALLSSFLAEQAQSPGLNQVGPPELLQRCQLEQKIATFENIVCLNREVERVAVTA 300
QY 222 EACSRQHRLDQDKIEALSCKVQQLERSIGLKDLAMADLEQKLEMEASTYDGVFIWKISD 281
DB 301 EACSRQHRLDQDKIEALSCKVQQLERSIGLKDLAMADLEQKLEMEASTYDGVFIWKISD 360
QY 342 LLRWPNQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVDMNTIASGCPFCFVSKMEA 401
DB 361 FTRKQEAQVAGTRPAIFSPAFYTSRYGKMLCRVYLNQVGPPELLQRCQLEQKIATFENIVCLNREVERVAVTA 420
QY 402 KNSYVRDDAIFKAIIVDLTGL 422
DB 481 KNSYVRDDAIFKAIIVDLTGL 501

RESULT 5
US-08-779-599-4

; Sequence 4, Application US/08779599

; Patent No. 6500922

; GENERAL INFORMATION:

; APPLICANT: Goeddel, David V.

; APPLICANT: Rothe, Mike

; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/779,599

; FILING DATE: 07-Jan-1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Ginger R.

; REGISTRATION NUMBER: 33,055

; REFERENCE/DOCKET NUMBER: P0897C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-3216

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 501 amino acids

; TYPE: Amino acid

; TOPOLOGY: Linear

; US-08-779-599-4

Query Match

Best Local Similarity 86.6%; Score 1914.5; DB 4; Length 501;

Mismatches 21; Indels 79; Gaps 1;

Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRPFOACGHRVCSFCLAS 60

DB 1 MAASVTPSGSLELLQPGFSKTLTGKLEAKYLCACRNILRRPFOACGHRVCSFCLTS 60

QY 61 ILSSGPQNCACVVEGLYEEGISESSAPPDNaARREVESLPVPCSDGCTWKGTLKE 120

DB 61 ILSSGPQNCACVVEGLYEEGISESSAPPDNaARREVESLPVPCSDGCTWKGTLKE 120

QY 121 YE----- 122

DB 121 YESCHEGLCPFLTECPACKGLVRLSEKHEHTEQECFKRSLSCQHCRAPCSHVLDLVHYE 180

QY 123 -----FQDHVKTGCKRVPFCRFAIGCLTVEGEKQOEHEVQWL 161

DB 181 VCPFPPLTDCGCKKIPRETQFQDHVRACSKRVLCRFHTVGCSEWVETENLQDHELQRL 240

QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNRVERVAVMTA 221

DB 241 REHLALLSSPLEAQAQSPGTINQVGPPELLQRCQILEQKIATFENIVCVLNRVERVAVMTA 300

QY 222 EACSRQRLDQDKTEALSSKVOQLERSIGLKDAMADLEQKLEMEASTYDGVFIKISD 281

DB 301 EACSRQRLDQDKTEALSNKVVQQLERSIGLKDAMADLEQKLEMEASTYDGVFIKISD 360

QY 282 PARKLQEAAGRIPIAFSPAFYTSRYGYKCLRIYLNQDGTGRGTHLSLFFVVMKGFNDA 341

DB 361 PTKRQEAAGRTPIAFSPAFYTSRYGYKCLRIYLNQDGTGRGTHLSLFFVVMKGFNDA 420

QY 342 LLRPFRNOKVTMLLDONNREHVDAFRPDVTSSSFQRPVNDNVIASGCLFPCVSKMEA 401

DB 421 LLQWPFNOKVTMLLDHNNREHVDAFRPDVTSSSFQRPVNDNVIASGCLFPCVSKMEA 480

QY 402 KNSYVRDDAIFIKAIIVDLTGL 422

DB 481 KNSYVRDDAIFIKAIIVDLTGL 501

RESULT 6

PCT-US95-06639-4

; Sequence 4, Application PC/TUS9506639

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/06639

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/250858

; FILING DATE: 27-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/331394

; FILING DATE: 28-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Ginger R.

; REGISTRATION NUMBER: 33,055

; REFERENCE/DOCKET NUMBER: 897P2PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-3216

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 501 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; PCT-US95-06639-4

Query Match 86.6%; Score 1914.5; DB 5; Length 501;

Best Local Similarity 74.3%; Pred. No. 6.4e-184;

Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRPFOACGHRVCSFCLAS 60

DB 1 MAASVTPSGSLELLQPGFSKTLTGKLEAKYLCACRNILRRPFOACGHRVCSFCLTS 60

QY 61 ILSSGPQNCACVVEGLYEEGISESSAPPDNaARREVESLPVPCSDGCTWKGTLKE 120

DB 61 ILSSGPQNCACVVEGLYEEGISESSAPPDNaARREVESLPVPCSDGCTWKGTLKE 120

QY 121 YE----- 122

DB 121 YESCHEGLCPFLTECPACKGLVRLSEKHEHTEQECFKRSLSCQHCRAPCSHVLDLVHYE 180

QY 123 -----FQDHVKTGCKRVPFCRFAIGCLTVEGEKQOEHEVQWL 161

DB 181 VCPFPPLTDCGCKKIPRETQFQDHVRACSKRVLCRFHTVGCSEWVETENLQDHELQRL 240

QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNRVERVAVMTA 221

DB 241 REHLALLSSPLEAQAQSPGTINQVGPPELLQRCQILEQKIATFENIVCVLNRVERVAVMTA 300

QY 222 EACSRHRLDODKIEALSSKVOQLERSIGLKDLAVADLEOKVLEMAESTYDGVFIWKISD 281
DB 301 EACSRHRLDODKIEALSSKVOQLERSIGLKDLAVADLEOKVLEMAESTYDGVFIWKISD 360
QY 282 FARKLQEA VAGRIPAFISPAFTSYRYGKXCLRIYVINGDGTGRGTHLSLFFVVMKGPND 341
DB 361 FTRKQEA VAGRIPAFISPAFTSYRYGKXCLRIYVINGDGTGRGTHLSLFFVVMKGPND 420
QY 342 LRLWPNQKVTMLLDONNREHVIDAFRDPVTSSSFQREVDNMTASGCLFCPVSKMEA 401
DB 421 LQWPNQKVTMLLDONNREHVIDAFRDPVTSSSFQREVDNMTASGCLFCPVSKMEA 480
QY 402 KNSYVRDDAIFIKAIVDLTGL 422
DB 481 KNSYVRDDAIFIKAIVDLTGL 501

RESULT 7

US-09-181-958-1
; Sequence 1, Application US/09181958
; Patent No. 6143507
; GENERAL INFORMATION:
; APPLICANT: Kehry, Marilyn R
; APPLICANT: Crute, Steven S
; TITLE OF INVENTION: High Throughput Compatible Assays for Receptor-TRAF
; FILE REFERENCE: 9 142 Nucl. Seq
; CURRENT APPLICATION NUMBER: US/09/181,958
; CURRENT FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 243
; TYPE: PRT
; ORGANISM: human
US-09-181-958-1

Query Match 53.3%; Score 1178; DB 3; Length 243;
Best Local Similarity 99.6%; Pred. No. 3.1e-110;

Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CESLEKKTATFENIVCVLNREVERVAMTAECRSQRLDODKIEALSSKVOQLERSIGLK 252
DB 1 CESLEKKTATFENIVCVLNREVERVAMTAECRSQRLDODKIEALSSKVOQLERSIGLK 60
QY 253 DLAMADLEQKLEMAESTYDGVFIWKISDFARKLQEA VAGRIPAFISPAFTSYRYGYKMC 312
DB 61 DLAMADLEQKLEMAESTYDGVFIWKISDFARKLQEA VAGRIPAFISPAFTSYRYGYKMC 120
QY 313 LRIYNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDONNREHVIDAFRDPV 372
DB 121 LRIYNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDONNREHVIDAFRDPV 180
QY 373 TSSSFQRPVNDMNIAAGCLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 422
DB 181 TSSSFQRPVNDMNIAAGCLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 230

RESULT 8

US-08-331-394-2
; Sequence 2, Application US/08331394
; Patent No. 5670319
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,394
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-331-394-2

Query Match 32.9%; Score 727; DB 1; Length 409;
Best Local Similarity 38.5%; Pred. No. 1.8e-64;

Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;

QY 85 LESSSAFPDAAAREVESLPAVCPSDG-----CTWKGTLEKEVEPDQHVTKCGKCR----- 134
DB 1 MASSAPDENEFPQGCPPAPCQDPSEPRVLCCT--ACLSENLRDDEDRICPKCRADNLHP 58
QY 135 -----VPCRPHAIGLETVEGEKQOEHEVQMLREHLAMLSSVLE 174
DB 59 VSPGSLPTQEKVHSDVAEABIMCFFAGVGCGSKGSPQSMQEHSEATSSSHLYLLAVLKE 118
QY 175 AKPLLQSGHAGSELLOR-----CES----- 195
DB 119 WKSPGSLNLSAPWALERNLSELQQAATGDLVDYRAPCCESQEBALQHLVKEK 176
QY 196 ----LEKKTATFENIVCVLNREVERVAMTAECRSQRLDODKIEALSSKVOQLERSIGL 251
DB 179 LLAQLEKLRVFANIVAVLNKEVEASHLAASIHQSOLDREHLLSLEQRVVLELQOTLAQ 238
QY 252 KDLAMADLEQKLEMAESTYDGVFIWKISDFARKLQEA VAGRIPAFISPAFTSYRYGYKM 311
DB 239 KDQVLGKLEHLSRLMEEAESFDGTLWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKL 298
QY 312 CLRIYNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDONNREHVIDAFRDP 371
DB 299 CLRIYNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDONNREHVIDAFRDP 358
QY 372 VTSSSFQRPVNDMNIAAGCLFCPVSKMEA-KNSYVRDDAIFIKAIVD 418
DB 359 LSSASFQRPQSETNVASGCLFPLFPLSKLQSPKIAVYKDDTMFLKCIYD 406

RESULT 9

US-08-250-858-2
; Sequence 2, Application US/08250858
; Patent No. 5708142
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 62


```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,858
FILING DATE: 27-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 409 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-250-858-2

```

[illegible]

RESULT 10

RESULTS
US-08-446-915-2
; Sequence 2, Application US/08446915
; Patent No. 5741667
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.

RESULT 11
US-08-744-139-2
; Sequence 2, Application US/08744139
; Patent No. 5869612
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,139
; FILING DATE: 31-Oct-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 05/27/1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P0897C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-744-139-2
Query Match 32.9%; Score 727; DB 2; Length 409;
Best Local Similarity 38.5%; Pred. No. 1.8e-64;
Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;
QY 85 LESSAAPPDAAARREVESLPVCPDGG---CTWKGTLKEYEFQDHVKTGCKR----- 134
Db 1 MASSSAPDENEFGCGPPAPCDPSEPRVLCCT--ACLSNLRDDEDRICPKCRADNLHP 58
QY 135 -----VPCRFHAIGCLETVGEKQOEHEVQWLREHLAMLLSSVLE 174
Db 59 VSPGSPLOTQEKVHSDVAEAEIMCFPAGVGCSFKGSPQSMOEHEATSSQSHLYLLAVLKE 118
QY 175 AKPLLDGQSHAGSELLQR-----CES----- 195
Db 119 WKSSPGSNLGSAPWALERNLSELQAAVEATGDLVDVCRAPCCESQEEALQHLVKEK 178
QY 196 ----LEKKTATFNIVCVLNREVERVAMTAACSRQHRDLDDQKIEALSCKVQQLERSIGL 251
Db 179 LLAQLEEKLRVFANIVAVLNKEVEASHLAAASIHQSOLDREHLLSLEQVRVVELOQTLLAQ 238
QY 252 KDLAMADLEQKVLMEASATVDGVFIWKISDPARKLQEAAGVAGRIPAIFSPAFYTSRYGYKM 311
Db 239 KDQVLKLEHSLRLMEASFDGTFLNKTNVTKRCHESVCGRTVSLFSPAFYTKYGYKL 298
QY 312 CLRIYNGDGTGRGTHLSLFFVVMKGNPDALLRPFPNQKVTMLLDQNNREHVIDAFRDP 371
Db 299 CLRLYLNGDGGSKKTHLSLFFIVIMRGYDALLPWPFRNKVTFMLLDQNNREHAIDAFRDP 358
QY 372 VTSSSFQRPVNDMNIAAGCLPFCPVSKMEA-KNSYVRDDDAIFKAIYD 418
:::||||| :: :||||| :: :||||| :: :||||| :: :||||| :: :|||||

Db 359 LSSASFQRPQSETNVASGCELPFFLSKLQSPFKHAYVXDDTMFLKCIYD 406
RESULT 12
US-08-779-599-2
; Sequence 2, Application US/08779599
; Patent No. 6500922
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,599
; FILING DATE: 07-Jan-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P0897C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-779-599-2
Query Match 32.9%; Score 727; DB 4; Length 409;
Best Local Similarity 38.5%; Pred. No. 1.8e-64;
Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;
QY 85 LESSAAPPDAAARREVESLPVCPDGG---CTWKGTLKEYEFQDHVKTGCKR----- 134
Db 1 MASSSAPDENEFGCGPPAPCDPSEPRVLCCT--ACLSNLRDDEDRICPKCRADNLHP 58
QY 135 -----VPCRFHAIGCLETVGEKQOEHEVQWLREHLAMLLSSVLE 174
Db 59 VSPGSPLOTQEKVHSDVAEAEIMCFPAGVGCSFKGSPQSMOEHEATSSQSHLYLLAVLKE 118
QY 175 AKPLLDGQSHAGSELLQR-----CES----- 195
Db 119 WKSSPGSNLGSAPWALERNLSELQAAVEATGDLVDVCRAPCCESQEEALQHLVKEK 178
QY 196 ----LEKKTATFNIVCVLNREVERVAMTAACSRQHRDLDDQKIEALSCKVQQLERSIGL 251
Db 179 LLAQLEEKLRVFANIVAVLNKEVEASHLAAASIHQSOLDREHLLSLEQVRVVELOQTLLAQ 238
QY 252 KDLAMADLEQKVLMEASATVDGVFIWKISDPARKLQEAAGVAGRIPAIFSPAFYTSRYGYKM 311
Db 239 KDQVLKLEHSLRLMEASFDGTFLNKTNVTKRCHESVCGRTVSLFSPAFYTKYGYKL 298
QY 312 CLRIYNGDGTGRGTHLSLFFVVMKGNPDALLRPFPNQKVTMLLDQNNREHVIDAFRDP 371
Db 299 CLRLYLNGDGGSKKTHLSLFFIVIMRGYDALLPWPFRNKVTFMLLDQNNREHAIDAFRDP 358
QY 372 VTSSSFQRPVNDMNIAAGCLPFCPVSKMEA-KNSYVRDDDAIFKAIYD 418
:::||||| :: :||||| :: :||||| :: :||||| :: :||||| :: :|||||

Db 359 LSSASFQRPQSETNVASGCLFFPLSLKQSPKHAYVVDKDTWFLKCIVD 406

RESULT 13
PCT-US95-06639-2
; Sequence 2, Application PC/TUS9506639
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06639
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331394
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-06639-2

Query Match 32.9%; Score 727; DB 5; Length 409;
Best Local Similarity 38.5%; Pred. No. 1.8e-64;
Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;
QY 85 LESSAFDPNARREVSPLAVCFSDG----CTWKGTLEKEVEFQDHVKTGCKR----- 134
Db 1 MASSAPDENEFQGCCPAPQDSESRVLCCT--ACLSNLRDDDEDRICPKCADNLHP 58
QY 135 -----VPCRFHAGLCTVEGSKQEHVEQVWHLREHMLLSVLE 174
Db 59 VSPGSLTQEKVHSDVAEAEIMCPFAGVGCSPQSGMOEHEATSQSHYLLAVLKE 118
QY 175 AKPLLGQSHAGSELLOR-----CES----- 195
Db 119 WKSPGSGNLGAPNALERNLSELOQAVENTGDEVDVCRAPCCSQBELAQLHLVKEK 178
QY 196 ----LEKKTATFENIVCVLNREVERVAMTAEACSRQHLRDOODKIEALSSKVOQLERSIGL 251
Db 179 LLAQLEKLRVFANIVAVLNKEVEASHALAAASHQSLDREHLLSLEQRWELQOTLAQ 238
QY 252 KDLAMADLEQKVLWEASTVDGVFIWKISDFARKLOEAVAGRPAIFSPAFYTSRYCYKM 311
Db 239 KDQVLKLESLRMEASDGTFLWKITNVRKCHESVCGRTVSUFSFPAFYTKYGYKL 298
QY 312 CLRTYLNQDGTGRGTHLSLFFVVMKGPNDALLRPFNQKVTLLMLLDQNNREHVIDAFRPD 371

Db 299 CURLYNGDGGKTKHLSLFIVIMRGYDALLPWFPRNKVTFMFLDQNNREHAIDAFRPD 358

QY 372 VTSSSFQRPVNDMIASGCLFPCPVSKMEA-KNSYVRDDAIFIKAIVD 418
Db 359 LSSASFQRPQSETNVASGCLFFPLSLKQSPKHAYVVDKDTWFLKCIVD 406

RESULT 14
US-08-697-610-2
; Sequence 2, Application US/08697610
; Patent No. 6172187
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: CD40 Associated Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/697,610
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/349,357
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-697-610-2

Query Match 32.4%; Score 717; DB 3; Length 543;
Best Local Similarity 34.9%; Pred. No. 2.9e-63;
Matches 184; Conservative 76; Mismatches 125; Indels 142; Gaps 23;
QY 16 QGPFKTLTGKLEKYLKACRVLRPPFOAQOCHRYCSPCLASILSSGPNCAACVHE 75
Db 36 QGQYKEKFKVT-VEQYKCKCHLVLCSPKQTECHRCSCMAALLSSSPFKTAC-QE 93
QY 76 GYBERGIGILSSSAPPDAAARREVSPLAVC--PSDQCTWKGTL----- 118
Db 94 SLVKDKV-----FKDNCCKREILALQIYCRNESRGCAEQTLGHLVHLKNDCHFE 145
QY 119 -----KE-----YEFODHYK-----TCGKCR--VP-----CRFHAJCC- 144
Db 146 LFCVAPDCKEYLRKDLRDHVEKACKYREATCSCKSQVPMIALQKHEDTDCPCVVVSCP 205
QY 145 ----LQTV---EKEQKQ--EHEVQWLRHLAML--LSSVLEAKPLLDGQSHAGSELQRC 193
Db 206 HKCSQVTLRSEGTNQIQAHEASAVQHVNLKENSLEKK-----VSLIQN- 254
QY 194 ESLEKKA--TFENIVCVLNREVER-----VAMTAEACS----- 225
Db 255 ESVEKNKSIQSLHNOICSFETIERQEMLRNNEKSLIHLQRVIDSOAEKLEKLDKBI 314

QY 226 RQHLDD-----KIEALSSKVOOLE-----RSIGL-----KDLAM 256
 Db 315 FRQWEEADSMKSVESLQNRVTELESVDKSGAGQVARNTGLLESQLSRHDQMLSVHDRL 374
 QY 257 ADLEQKVLMEASTYDGVFIWKISDFARKLOEAVAGRIPAFSPAFYTSRYGYKMCRLRY 316
 Db 375 ADMDLRFQVLETASYNGVLWKIRYKRRKQEAVMGKTLISYQPFYTYGYKMCARVY 434
 QY 317 LMGDTGRTGTHLSLFFVVMKGPNDALLRPFNQKVTLMLLDQ--NNREHVIDAFRPDVTSS 375
 Db 435 LMGDMGKGTHTLSLFFVVMRGEYDALLPWPFPKQKVTLMMDQSSRRRLGDAFKDPDPS 494
 QY 376 SFQRPVNDMNIAAGCPLFCFVSKMEAKNSVYRDDAIFIKAIVDLTGL 422
 Db 495 SFKPTGEMNIAAGCPVFVAQTGLE-NGTYIKDDTIFIKVIVDTSD 540

RESULT 15

US-08-349-357-2
 ; Sequence 2, Application US/08349357
 ; Patent No. 6285556
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; APPLICANT: Sato, Takaaki
 ; TITLE OF INVENTION: CD40 Associated Proteins
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/349,357
 ; FILING DATE: 02-DEC-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LJ 1203
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 543 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-349-357-2

Query Match 32.4%; Score 717; DB 3; Length 543;
 Best Local Similarity 34.9%; Pred. No. 2,9e-63;
 Matches 184; Conservative 76; Mismatches 125; Indels 142; Gaps 23;
 QY 16 QPGFSKTLGTLEAKYLCSACRNVLRRPFAQCGRHYCSFCLASTLSSGPQNCACVHE 75
 Db 36 QGGYKEKFKVT-VEDKYKCEKHLVLCSPKQTECGHRSCECMAALLSSSPKCTAC-QE 93
 QY 76 GIYEGISILLESSAFPDNAAREVESLPVC--PSDGGCTWKGL-----118
 Db 94 SIVKDY-----FDNCCREILALQIYCNESRGCAEQTLGHLVLVHNDCHFEE 145
 QY 119 -----KE-----YBFQHVK-----TGKCR--VP-----CRFHAIGC- 144
 Db 146 LPCVRPCKEKVLRLDRDHVERACKYREATCSHCKSQVFMIALQKHEDTDCPCVVVSCP 205

QY 145 -----LETV---EGEKQ--EHEVQWREHLAML--LSSVLEAKPLLGDSHAGSELLQRC 193
 Db 206 HKGSVQTLRSEGTNOQIKAEASASSAVQHVNLKKEWSNLEKK-----VSJLQN- 254
 QY 194 ESLEKKTAT--TFENIVCVLNREVER-----VAMTABACS-----225
 Db 255 ESEKKNKSIQSLHNQICSEFIEIERQKEMLRNNESKILHLQRVIDSQAELKELDKEIRS 314
 QY 226 -RQHLDDQ-----KIEALSSKVOOLE-----RSIGL-----KDLAM 256
 Db 315 FRQWEEADSMKSVESLQNRVTELESVDKSGAGQVARNTGLLESQLSRHDQMLSVHDRL 374
 QY 257 ADLEQKVLMEASTYDGVFIWKISDFARKLOEAVAGRIPAFSPAFYTSRYGYKMCRLRY 316
 Db 375 ADMDLRFQVLETASYNGVLWKIRYKRRKQEAVMGKTLISYQPFYTYGYKMCARVY 434
 QY 317 LMGDTGRTGTHLSLFFVVMKGPNDALLRPFNQKVTLMLLDQ--NNREHVIDAFRPDVTSS 375
 Db 435 LMGDMGKGTHTLSLFFVVMRGEYDALLPWPFPKQKVTLMMDQSSRRRLGDAFKDPDPS 494
 QY 376 SFQRPVNDMNIAAGCPLFCFVSKMEAKNSVYRDDAIFIKAIVDLTGL 422
 Db 495 SFKPTGEMNIAAGCPVFVAQTGLE-NGTYIKDDTIFIKVIVDTSD 540

Search completed: November 10, 2004, 16:29:44
 Job time : 42 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2004, 16:28:24 ; Search time 143 seconds

(without alignments)
1042.387 Million cell updates/sec

Title: US-10-018-030b-2

Perfect score: 2211

Sequence: 1 MAASVTPPGSLELLQPGFS.....NSYVRDDAIFKAIVDLTGL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata1/pubpaa/PTC_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata1/pubpaa/PTC_US_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata1/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2047.5	92.6	501	15 US-10-361-270-1	Sequence 1, Appli
2	1914.5	86.6	501	14 US-10-283-500-4	Sequence 4, Appli
3	1831.5	73.8	477	14 US-10-094-749-1702	Sequence 1702, Ap
4	730	33.0	586	8 US-08-813-323A-1	Sequence 1, Appli
5	727	32.9	409	14 US-10-283-500-2	Sequence 2, Appli
6	722	32.7	543	14 US-10-004-378A-35	Sequence 35, Appli
7	717.5	32.5	568	8 US-08-813-323A-2	Sequence 2, Appli
8	717.5	32.5	568	14 US-10-116-275-173	Sequence 173, App
9	717.5	32.5	568	14 US-10-004-378A-36	Sequence 36, Appli
10	717	32.4	543	9 US-09-757-041-2	Sequence 2, Appli
11	713.5	32.3	568	15 US-10-042-865-166	Sequence 166, App
12	710	32.1	567	14 US-10-242-212-7	Sequence 7, Appli
13	710	32.1	567	14 US-10-207-655-103	Sequence 103, App

14	687.5	31.1	538	15 US-10-042-865-163	Sequence 163, App
15	687.5	31.1	557	14 US-10-004-378A-34	Sequence 34, Appli
16	687.5	31.1	557	15 US-10-042-865-162	Sequence 162, App
17	686	31.0	568	15 US-10-262-445-132	Sequence 132, Appli
18	686	31.0	568	15 US-10-042-865-38	Sequence 38, Appli
19	679.5	30.7	438	9 US-09-950-902-2	Sequence 2, Appli
20	674.5	30.5	417	14 US-10-453-478-18	Sequence 18, Appli
21	664.5	30.1	451	14 US-10-004-378A-2	Sequence 2, Appli
22	664	30.0	526	15 US-10-262-445-130	Sequence 130, Appli
23	664	30.0	526	15 US-10-042-865-50	Sequence 50, Appli
24	664	30.0	558	14 US-10-004-378A-32	Sequence 32, Appli
25	664	30.0	558	15 US-10-042-865-164	Sequence 164, App
26	659	29.8	558	14 US-10-004-378A-33	Sequence 33, Appli
27	659	29.8	558	15 US-10-042-865-165	Sequence 165, App
28	638	28.9	347	9 US-09-950-902-4	Sequence 4, Appli
29	621	28.1	386	14 US-10-004-378A-4	Sequence 4, Appli
30	457.5	20.7	143	14 US-10-004-378A-38	Sequence 38, Appli
31	424	19.2	530	15 US-10-042-865-131	Sequence 131, App
32	410	18.5	522	15 US-10-042-865-129	Sequence 129, App
33	408	18.5	522	15 US-10-042-865-130	Sequence 130, App
34	378	17.1	526	15 US-10-042-865-24	Sequence 24, Appli
35	255	11.5	131	15 US-10-131-487A-61	Sequence 61, Appli
36	249.5	11.3	72	9 US-09-864-761-3393	Sequence 3393, A
37	206	9.3	43	9 US-09-798-789-3	Sequence 3, Appli
38	206	9.3	43	9 US-09-981-889-3	Sequence 3, Appli
39	206	9.3	43	14 US-10-262-630-25	Sequence 25, Appli
40	198	9.0	399	15 US-10-042-865-132	Sequence 132, App
41	165.5	7.5	61	9 US-09-796-692-857	Sequence 857, App
42	185.5	7.5	61	14 US-10-040-862-857	Sequence 857, App
43	185.5	7.5	61	15 US-10-057-475B-857	Sequence 857, App
44	185.5	7.5	61	15 US-10-154-884B-857	Sequence 857, App
45	165.5	7.5	61	16 US-10-764-324-857	Sequence 857, App

ALIGNMENTS

RESULT 1
US-10-361-270-1
; Sequence 1, Application US/10361270
; Publication No. US20040038299A1
; GENERAL INFORMATION:
; APPLICANT: Kuai, Jun
; APPLICANT: Wocters, Joseph L
; APPLICANT: Nickbarg, Elliott
; APPLICANT: Qiu, Yongchang
; APPLICANT: Lin, Lih-Ling
; TITLE OF INVENTION: Composition and Method for Modulating an Inflammatory
; TITLE OF INVENTION: Response
; FILE REFERENCE: 22058-565
; CURRENT APPLICATION NUMBER: US/10/361,270
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/355,183
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-270-1

Query Match 92.6%; Score 2047.5; DB 15; Length 501;
Best Local Similarity 80.4%; Pred. No. 7e-173;
Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;

QY 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRPFOACGHRYSFCFLAS 60
DB 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRPFOACGHRYSFCFLAS 60

QY 61 ILSSGPQNCACVHEGYEEGISESSAPPDNAAREVESLFAVCPSCDCTWKGLTKE 120
DB 61 ILSSGPQNCACVHEGYEEGISESSAPPDNAAREVESLFAVCPSCDCTWKGLTKE 120

QY 121 YE-----122
 Db 121 YESCHGRCPLMLTECPACKGLVRLGKERHLEHECPERSLSCHRCAPCGADVKAHHE 180
 QY 123 -----FQHVTKGCRVPCRFPAHIGCLTVEGEKQHEVQWL 161
 Db 181 VCPKPLTCDGCKKKIPREXFDHVTKGCRVPCRFPAHIGCLTVEGEKQHEVQWL 240
 QY 162 REHLAMLVSSVLEAKPLGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221
 Db 241 REHLAMLVSSVLEAKPLGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 300
 QY 222 EACSRQHLDDQKIEALSQVQLERSIGLKDLMADLEQKVLMEASTYDGVFIWKISD 281
 Db 301 EACSRQHLDDQKIEALSQVQLERSIGLKDLMADLEQKVLMEASTYDGVFIWKISD 360
 QY 282 FARKLOEAVAGRIPAIFSPAFYTSRYGYMCLIRIYNGDGTGRGTHLSLFFVVMKGNDA 341
 Db 361 ILRLQOEAVAGRIPAIFSPAFYTSRYGYMCLIRIYNGDGTGRGTHLSLFFVVMKGNDA 420
 QY 342 LLRWPFNKQVTLMLDDQNNRHHVIDAFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA 401
 Db 421 LLRWPFNKQVTLMLDDQNNRHHVIDAFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA 480
 QY 402 KNSYVRDDAIFIKAIVDLTGL 422
 Db 481 KNSYVRDDAIFIKAIVDLTGL 501
 RESULT 2
 US-10-283-500-4
 ; Sequence 4, Application US/10283500
 ; Publication No. US20030120043A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goeddel, David V.
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/283,500
 ; FILING DATE: 30-Oct-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/779,599
 ; FILING DATE: 07-Jan-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dregler, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: P0897C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-3216
 ; TELEFAX: 415/225-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 501 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-283-500-4

Query Match 86.6%; Score 1914.5; DB 14; Length 501;
 Best Local Similarity 74.3%; Pred. No. 4.5e-161;
 Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;
 QY 1 MAAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRPFAQCCHRYCSFCLAS 60
 Db 1 MAAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRPFAQCCHRYCSFCLAS 60
 QY 61 ILSSGPNQCAACVHEGIEEGISILESSAPPDNAARREVESLPVCPSDGCTWKGTLKE 120
 Db 61 ILSSGPNQCAACVHEGIEEGISILESSAPPDNAARREVESLPVCPSDGCTWKGTLKE 120
 QY 121 YE-----122
 Db 121 YESCHGRCPLMLTECPACKGLVRLGKERHLEHECPERSLSCHRCAPCGADVKAHHE 180
 QY 123 -----FQHVTKGCRVPCRFPAHIGCLTVEGEKQHEVQWL 161
 Db 181 VCPKPLTCDGCKKKIPREXFDHVTKGCRVPCRFPAHIGCLTVEGEKQHEVQWL 240
 QY 162 REHLAMLVSSVLEAKPLGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221
 Db 241 REHLAMLVSSVLEAKPLGDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 300
 QY 222 EACSRQHLDDQKIEALSQVQLERSIGLKDLMADLEQKVLMEASTYDGVFIWKISD 281
 Db 301 EACSRQHLDDQKIEALSQVQLERSIGLKDLMADLEQKVLMEASTYDGVFIWKISD 360
 QY 282 FARKLOEAVAGRIPAIFSPAFYTSRYGYMCLIRIYNGDGTGRGTHLSLFFVVMKGNDA 341
 Db 361 ILRLQOEAVAGRIPAIFSPAFYTSRYGYMCLIRIYNGDGTGRGTHLSLFFVVMKGNDA 420
 QY 342 LLRWPFNKQVTLMLDDQNNRHHVIDAFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA 401
 Db 421 LLRWPFNKQVTLMLDDQNNRHHVIDAFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA 480
 QY 402 KNSYVRDDAIFIKAIVDLTGL 422
 Db 481 KNSYVRDDAIFIKAIVDLTGL 501
 RESULT 3
 US-10-094-749-1702
 ; Sequence 1702, Application US/10094749
 ; Publication No. US20030219741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKABATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOHICO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOYUKI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
 ; FILE REFERENCE: 084335/0160
 ; CURRENT APPLICATION NUMBER: US/10/094,749
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/350,435
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: JP 2001-328381
 ; PRIOR FILING DATE: 2001-09-14


```

; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1702
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-094-749-1702

Query Match
Best Local Similarity 73.8%; Score 1631.5; DB 14; Length 447;
Matches 340; Conservative 17; Mismatches 50; Indels 55; Gaps 9;

QY 1 MAASVTPPGSLELLQFGSKTLTGKLEAKYLCACRNVLRRPFOAQCGHYCSFCLAS 60
DB 1 MAASVTPPGSLELLQFGSKTLTGKLEAKYLCACRNVLRRPFOAQCGHYCSFCLAS 60
QY 61 ILSSGPNCAACVHEGIYEGISILESSAFPDNAARREVESLPVCPDGGCTWKGTLE 120
DB 61 ILSSGPNCAACVHEGIYEGISILESSAFPDNAARREVESLPVCPDGGCTWKGTLE 120
QY 121 YFQDHFVKTG-----KCRVPCRTHAI-----GLETVEGEKQEHVQWL 161
DB 121 YEVK--MPACGMWTEAPVAGSRPRSPSSVDLVHPLTGAECALMSVEETE----- 170
QY 162 REHMLLSVLEAK-PL-----LGD-QSHAGSELLQRCSELEKKTATFENI 206
DB 171 -----LLRSCHGRCPLMLTECPACKGLVRLGEKERHLEHECPERSLSCHRCRAPCCGA 225
QY 207 VCVLNEV-ERVAMTAEACS-----RQRLDQDKIEALSKVQCLERSIGLKLAMADLE 260
DB 226 DVKAHEVCPKPLTCDGCKKIKPREKFDQDQKIEALSKVQCLERSIGLKLAMADLE 285
QY 261 QKLEMEASTYDGVFIWKISDFARKLQEAAGRIAPAFSPAFYTSRYGKMCIRIYNGD 320
DB 286 QKLEMEASTYDGVFIWKISDFARKLQEAAGRIAPAFSPAFYTSRYGKMCIRIYNGD 345
QY 321 GTGRGTHLSLFFVVMKGPNDALLRPFNOKVTMLMLDQNNREHVIDAFRPDVTSSSFQRP 380
DB 346 GTGRGTHLSLFFVVMKGPNDALLRPFNOKVTMLMLDQNNREHVIDAFRPDVTSSSFQRP 405
QY 381 VNDMNIASGCPFLCPVSKMEAKNSYVRDDAIFIKAVIDLTLGL 422
DB 406 VNDMNIASGCPFLCPVSKMEAKNSYVRDDAIFIKAVIDLTLGL 447

```

```

RESULT 4
US-08-813-323A-1
; Sequence 1, Application US/0881323A
; Publication No. US20020031522A1
; GENERAL INFORMATION:
; APPLICANT: Baltimore, David
; APPLICANT: Cheng, Genhong
; APPLICANT: Cleary, Aileen
; APPLICANT: Lederman, Seth
; APPLICANT: Ye, Zheng-sheng
; TITLE OF INVENTION: TRUNCATED CRAF1 INHIBITS CD40 SIGNALING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/813,323A
; FILING DATE:
; CLASSIFICATION: 530

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50659
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 566 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..566
; US-08-813-323A-1

Query Match
Best Local Similarity 33.0%; Score 730; DB 8; Length 566;
Matches 187; Conservative 80; Mismatches 111; Indels 184; Gaps 22;

QY 1 MAASVTPPGSLELLQ-----GFSKTLTGKLEAKYLCACRNVLRRPFOA 47
DB 7 MDAAGTLQNPPLKQPDGAGSVLPVPEQGGYKEKFKVT-VEKYKCEKRLVLCNPKQT 65
QY 48 QGHRYSFCFLASILLSSGPONCAACVHEGIYEGISILESSAFPDNAARREVESLPVAVC 107
DB 66 ECGHRFCSCMAILLSSSSPKCTAC-QESIINKDV-----FKDNCCREIALLQVYC 116
QY 108 PSD--GCTWKGTL-----KEYEFO-----DHVK-----TC 130
DB 117 RNEGRCGAEQLTGLHLLVHLKNEQFELPCLRADCKEKLRLKDLRDHVEKACKYREATC 176
QY 131 GKCR--VP-----CRFEAI 142
DB 177 SHKSVQPMIKLQKHEDTDCPVVSCPHKCSVQTLRSELSELSAHLSECVNAPSTCSFAY 236
QY 143 GCLETVEGEKQ--EHEVQWLREHLAML--LSSVLEAKPLLGDSHAGSELLQRCSELEK 198
DB 237 GCV--FQGTNQIKAHEASSAVQHVLLKWSNSLEKK-----VSLQN-ESVEK 283
QY 199 KTA--TFENIVCVLNREVER-----VAMTAEACS-----FQHR 229
DB 284 NKSQSLHNQICSPFEIERQKEMLRNNEKILHLQRLVIDSQAEKLEKDEKIRPFQNW 343
QY 230 LDQD-----KIEALSKVQCLERSIGLKLAMADLE 261
DB 344 EADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQLSRHDQTLSDHDIRLADMDL 403
QY 262 KYLEMEASTYDGVFIWKISDFARKLQEAAGRIAPAFSPAFYTSRYGKMCIRIYNGD 321
DB 404 RFQVLETAHYNGVLIWKIRYKRRKQEAVMGKTLISYSQPPYTGFGYKMCARYLNGD 463
QY 322 TGRGTHLSLFFVVMKGPNDALLRPFNOKVTMLMLDQ--NNREHVIDAFRPDVTSSSFQRP 380
DB 464 MKGTHLSLFFVIMRGEVDALLPFPFKQKVTMLMLDQSSRRHLGDAFKPDPSNSSFQKP 523
QY 381 VNDMNIASGCPFLCPVSKMEAKNSYVRDDAIFIKAVIDLTLGL 422
DB 524 TGMNIASGCPFVFAQTVLE-NGTVIKDDTIFIKVIDTSDL 564

RESULT 5
US-10-283-500-2
; Sequence 1, Application US/10283500
; Publication No. US20030120043A1
; GENERAL INFORMATION:
; APPLICANT: Goettel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 59

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/283,500
;; FILING DATE: 30-Oct-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/779,599
;; FILING DATE: 07-Jan-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dreger, Ginger R.
;; REGISTRATION NUMBER: 33,055
;; REFERENCE/DOCKET NUMBER: P0897C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-3216
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;;
;; INFORMATION FOR SEQ ID NO: 2:
;;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 409 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-283-500-2

Query Match 32.9%; Score 727; DB 14; Length 409;
Best Local Similarity 38.5%; Pred. No. 1e-55;
Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;

QY 85 LESSAFPDNAARREVESLPVCPDSG-----CTWKGLKEYEFODHVKTCKCK-----134
DB 1 MASSSAPDENEFQFCPPAPQDPSEPRVLCT--ACLSENLRDDEDRICPKCRADNLHP 58
QY 135 -----VPCRHAIGCLETVEGEKQOEHEVQWLEHMLLSVLE 174
DB 59 VSPGSLTQEKVSHDVAEABIMCPPAGVGCSPQSMQHEATSSSHLYLLAVLKE 118
QY 175 AKPLIGDQSHAGSELLOR-----CES-----195
DB 119 WKSPGSLGAPNALERNLSLQLOAAVEATGDLVDVCPACCSQBELALQHLVKEK 178
QY 196 ----LEKTAFTENIVCVLNREVERVAMTACRQRHLRDLQKLEALSSKQVQLERISGL 251
DB 179 LLAQLEELRVANIVAVLNKEVEASHALAAASHQSLDRHLLSLQEVVELQQTQAQ 238
QY 252 KDLAMADLEQKLEWASTYGVFWKISDFARKLQEAQVAGRIAPFSPAFYTSRYGYKM 311
DB 239 KDQVGLKLESLRLMEBASFGTFLWKITNTKCHESVCGRTVSLSPAFYAKYGYKL 298
QY 312 CLRILYNGDGTGRGTHLSLFFVVMKGNDAALLRPFPKQVTLMLLDQNNREHVIDAFRPD 371
DB 299 CLRILYNGDGSKKTHLSLFLVIMRGEDALLPWFPRFNKVTFLMLDQNNREHAIDAFRPD 358
QY 372 VTSSSFQRPVNDMNTASCPFLFCPVSKWEA-KNSYVRRDDAIFIKAIYD 418
DB 359 LSSASFQRPVNETNASCCPLFFFLSLKQSPKHAIVKDDTNFLKCIYD 406

RESULT 6
US-10-004-378A-35
; Sequence 35, Application US/10004378A
; Publication No. US20030228301A1
; GENERAL INFORMATION:

;; APPLICANT: Li, Li
;; APPLICANT: Furtak, Kazarzyna
;; APPLICANT: Ferna, Amanda
;; APPLICANT: Patturajan, Meera
;; APPLICANT: Shimkets, Richard A
;; APPLICANT: Guo, Xiaojia Sasha
;; APPLICANT: Casman, Stacie J
;; APPLICANT: Burgess, Catherine E
;; APPLICANT: Malyankar, Uriel M
;; APPLICANT: Tchernev, Velizar T
;; APPLICANT: Vernet, Corinne A
;; APPLICANT: Spytek, Kimberly A
;; APPLICANT: Agee, Michele
;; APPLICANT: Rastelli, Luca
;; APPLICANT: Shenoy, Suresh G
;; APPLICANT: Grosse, William M
;; APPLICANT: Alsbrook II, John P
;; APPLICANT: Lepley, Denise M
;; APPLICANT: Gerlach, Valerie
;; APPLICANT: Edinger, Schlomit
;; APPLICANT: MacDougall, John R
;; APPLICANT: Peyman, John A
;; APPLICANT: Gunther, Erik
;; APPLICANT: Stone, David J
;; APPLICANT: Ellerman, Karen
;; APPLICANT: Gangolli, Esha A
;; TITLE OF INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides Encoding The
;; TITLE OF INVENTION: Methods of Using the Same
;; FILE REFERENCES: 21402-179
;; CURRENT APPLICATION NUMBER: US/10/004,378A
;; CURRENT FILING DATE: 2001-10-24
;; PRIOR APPLICATION NUMBER: 60/242,882
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: 60/242,765
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: 60/300,206
;; PRIOR FILING DATE: 2001-06-22
;; PRIOR APPLICATION NUMBER: 60/242,789
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: 60/242,768
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: 60/242,767
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: 60/243,622
;; PRIOR FILING DATE: 2000-10-26
;; PRIOR APPLICATION NUMBER: 60/273,047
;; PRIOR FILING DATE: 2001-03-02
;; PRIOR APPLICATION NUMBER: 60/243,591
;; PRIOR FILING DATE: 2000-10-26
;; PRIOR APPLICATION NUMBER: 60/243,950
;; PRIOR FILING DATE: 2000-10-27
;; Remaining prior application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 191
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 35
;; LENGTH: 543
;; TYPE: PPT
;; ORGANISM: Homo sapiens
US-10-004-378A-35

Query Match 32.7%; Score 722; DB 14; Length 543;
Best Local Similarity 34.9%; Pred. No. 4.1e-55;
Matches 184; Conservative 77; Mismatches 124; Indels 142; Gaps 23;

QY 16 QGFSKTLTGKLEAKYLCSACRNVLRPFOACQCHRYCSCCLASILSSGPNCAACVHE 75
DB 36 QGGYKEKFKVT-VEKYKCEKCHLVLCSPKQTECHRCFESCMALJSSSSPKTAC-QE 93
QY 76 GIYEGISILESSSAFPDAAARREVESLPVAVC--PSDQCTWKGL-----118
DB 94 SIVKDKV-----FKDNCCKREILALQIYCRNESRCAEQTLTLHLVHLKNDCHFE 145
QY 119 -----KE-----YEFQDHVK-----TCGKCR---VP-----CRFHAIGC- 144


```

Matches 194; Conservative 75; Mismatches 124; Indels 171; Gaps 22;
QY 16 QGFSKTLTGKLEAKYLCACRNVLRRPFOAQOCHRYCSFCLASILLSSGPNCAACVHE 75
Db 36 QGYSKTLTGKLEAKYLCACRNVLRRPFOAQOCHRYCSFCLASILLSSGPNCAACVHE 75
QY 76 GYIEGISTLESSAPPNAAAREVESLPVAV--PSDGTWKGT----- 118
Db 94 SIVKQV-----FKDCKCKREILALQIYCRNESRGCAEQTLGLHLLVHLKNDCHFEE 145
QY 119 -----KE-----YEFQDHVK-----TCGKCR--VP----- 136
Db 146 LPCVRPDCCKEVLKDLRDHVEKACKYREATCSHCQSQVPMIALQKHEDTDCPCVVVSCP 205
QY 137 -----CRFHAIGCLTVEGEKQO--EHEVQWLREHLAML 168
Db 206 HKCSVQTLRLSELSEHSECVNAPSTCSFKRYGCV--FQGTNQIQAHAESSAVQHVNL 263
QY 169 --LSSVLEAKPLLDQSHAGSELQRCESLEKTA--TFENIVCVLNEVER----- 216
Db 264 KEWSNSLEKK-----VSLQN--ESVEKNKSIQSLHNQICSFTEIERQKEMLRNN 312
QY 217 -----VAMTAEACS-----RQRLDQD-----KIEALSSKVQOLE----- 246
Db 313 ESKILHLQVIDSQAEKLEKLDKEIRPPQNWEEADSMKSSVESLQNRVTELESVDKSAG 372
QY 247 ---RSIGL-----KDLAMADLEQKLEMEASTYDGVFIWKISDFARKLQEA 289
Db 373 QVARTGLLESQSLSRDQMSVHDIRLADMDLRVQLVETASYNGLVWKIRYKRRQEA 432
QY 290 VAGRIPAIFSPAFYTSRYGKMCRLIYNGDGTGRGTHLSLFFVVMKGPNDALLRPFPQ 349
Db 433 VMGKTLISYQPFYTGFGYKMCARVYNGDMGKGTLSLFFVIMRGEVDALLPWFQK 492
QY 350 KVTMLLDQ--NNREHVIDAFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEAKNSYVRD 408
Db 493 KVTMLMDQSSRRHLGDAFPDNPSSSFKPTGEMNIAAGCPLFCPVSKMEAKNSYVRD 551
QY 409 DAIFKAIVDLTGL 422
Db 552 DTIFKIVIDTSDL 565

RESULT 9
US-10-004-378A-36
; Sequence 36, Application US/10004378A
; Publication No. US20030228301A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Furtak, Kazarzyna
; APPLICANT: Perna, Amanda
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard A
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Casman, Stacie J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Tchernov, Velizar T
; APPLICANT: Vernet, Corrine A
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Agee, Michele
; APPLICANT: Rastelli, Luca
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Gerlach, Valerie
; APPLICANT: Edinger, Schlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Peyman, John A
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David J
; APPLICANT: Ellerman, Karen

```

```

; APPLICANT: Gangolli, Esha A
; TITLE OF INVENTION: No. US20030228301A1 Human Proteins, Polynucleotides Encoding The
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 21402-179
; CURRENT APPLICATION NUMBER: US/10/004,378A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/242,882
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,765
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/300,206
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/242,789
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,768
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,767
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/243,622
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/273,047
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/243,591
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/243,950
; PRIOR FILING DATE: 2000-10-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-004-378A-36

Query Match 32.5%; Score 717.5; DB 14; Length 568;
Best Local Similarity 33.2%; Pred. No. 1.1e-54;
Matches 194; Conservative 75; Mismatches 124; Indels 171; Gaps 22;

QY 16 QGFSKTLTGKLEAKYLCACRNVLRRPFOAQOCHRYCSFCLASILLSSGPNCAACVHE 75
Db 36 QGYSKTLTGKLEAKYLCACRNVLRRPFOAQOCHRYCSFCLASILLSSGPNCAACVHE 75
QY 76 GYIEGISTLESSAPPNAAAREVESLPVAV--PSDGTWKGT----- 118
Db 94 SIVKQV-----FKDCKCKREILALQIYCRNESRGCAEQTLGLHLLVHLKNDCHFEE 145
QY 119 -----KE-----YEFQDHVK-----TCGKCR--VP----- 136
Db 146 LPCVRPDCCKEVLKDLRDHVEKACKYREATCSHCQSQVPMIALQKHEDTDCPCVVVSCP 205
QY 137 -----CRFHAIGCLTVEGEKQO--EHEVQWLREHLAML 168
Db 206 HKCSVQTLRLSELSEHSECVNAPSTCSFKRYGCV--FQGTNQIQAHAESSAVQHVNL 263
QY 169 --LSSVLEAKPLLDQSHAGSELQRCESLEKTA--TFENIVCVLNEVER----- 216
Db 264 KEWSNSLEKK-----VSLQN--ESVEKNKSIQSLHNQICSFTEIERQKEMLRNN 312
QY 217 -----VAMTAEACS-----RQRLDQD-----KIEALSSKVQOLE----- 246
Db 313 ESKILHLQVIDSQAEKLEKLDKEIRPPQNWEEADSMKSSVESLQNRVTELESVDKSAG 372
QY 247 ---RSIGL-----KDLAMADLEQKLEMEASTYDGVFIWKISDFARKLQEA 289
Db 373 QVARTGLLESQSLSRDQMSVHDIRLADMDLRVQLVETASYNGLVWKIRYKRRQEA 432
QY 290 VAGRIPAIFSPAFYTSRYGKMCRLIYNGDGTGRGTHLSLFFVVMKGPNDALLRPFPQ 349
Db 433 VMGKTLISYQPFYTGFGYKMCARVYNGDMGKGTLSLFFVIMRGEVDALLPWFQK 492
QY 350 KVTMLLDQ--NNREHVIDAFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEAKNSYVRD 408

```

Db 493 KVTMLMDQSGRRRLHGLDAFKDPDNNSSPKPTGEMNIASGCPVFAQTIVLE-NGTYIKD 551
QY 409 DAIFKAIYDITGL 422
Db 552 DIIFKIVDITSD 565

RESULT 10
US-09-757-041-2
; Sequence 2, Application US/09757041
; Patent No. US20020009726A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: CD40 Associated Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/757,041
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/349,357
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-757-041-2

Query Match 32.4%; Score 717; DB 9; Length 543;
Best Local Similarity 34.8%; Pred. No. 1.1e-54;
Matches 184; Conservative 76; Mismatches 125; Indels 142; Gaps 23;

QY 16 QPGSKTLTGKLEAKYLKACNVLRRPFOAQCGHYRCSFCLASTLSSGPQNCACVHE 75
Db 36 QGYSKEKFKVT-VEKYKCKCHLVLCSPKQTECHGRSCSCWAALLSSSPKCTAC-QE 93
QY 76 GIYBEGISILESSAFDPAAREVESLPVC--PSDGGCTWKTGL----- 118
Db 94 SIYKDKV-----FDKNCCKREILALQIYCRNESRGCAEQLTGLHLVLKNDCHFE 145
QY 119 -----KE---YEFQDHVK-----TCKGCR--VP-----CRFHAIGC- 144
Db 146 LPCRVDCKEKVLKDLRDEKACKYREATCSHCKSQVPMALQKHEDTDCFCVVVSCP 205
QY 145 -----LETV-----EGEKQO---EHEVQVLRHLAML--LSSVLEAKPLIGDQSHAGSELLQRC 193
Db 206 HKCSVQTLRSEGTNOQIKAHASSAVQVNLKWSNLEKK-----VSLQK- 254
QY 194 ESLEKKA--TFENIVCVLNRVER-----VAMTAEACS----- 225
Db 255 ESVEKNKIQSLNQKSCFEIEROKEMLRNNEKILHLQVIDSQAEKLEKLEKRS 314

QY 226 -RQRLDQD-----KIEALSSKVOOLE-----RSIGL-----KDLAM 256
Db 315 FRQWEEADSMKSSVESLQNRVTELESVDKSAQGVARTNTGLLESQLSRHDQMLSVHDRL 374
QY 257 ADLEQKULENEASTYDQVFIWKISDFARKLOEAVAGRIPAIFSPAFYTSYGYKXCLRIY 316
Db 375 ADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLISLSYQFFYTYGYGKMCARVY 434
QY 317 LNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNOKVTLMLLDQ--NNREHVIDAFRPDVTSS 375
Db 435 LNGDMGKGTHTLSLFFVIMRGEVDALLPWFPKQKVTMLMDQSGRRRLHGLDAFKDPDSS 494
QY 376 SFQRPVNDMNIASGCPFCPSVKMEAKNSYVRDADIPIKAIYDITGL 422
Db 495 SFKKPTGEMNIASGCPVFAQTIVLE-NGTYIKDDTIFIKIVDITSD 540

RESULT 11
US-10-042-865-166
; Sequence 166, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Sarence L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 166
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-042-865-166

Query Match 32.3%; Score 713.5; DB 15; Length 568;
Best Local Similarity 32.7%; Pred. No. 2.5e-54;
Matches 181; Conservative 75; Mismatches 127; Indels 171; Gaps 21;

QY 16 QGFSKTLTGKLEAKYLCSACNVLRPFOACQCHRYCSFCLASILSSGPONCAACVHE 75
DB 36 QGGYKEKFKVT-VEKYKCEKCHLVLCSPKQTECHRFCECMAALLSSSPKCTAC-QE 93
QY 76 GIYEGISILESSAPPDNAARREVESLPAVC--PSDGT-----113
DB 94 SIVKDKV-----FKDNCKREILALQIYCRNESRGCAEQMLGLHLVHLKNDCHFEEL 145
QY 114 -----WKGTLKEYEFQDHVK-----TCGKCR--VP-----136
DB 146 PCVRPDCKEKVLKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDPCVVVSCP 205
QY 137 -----CRFHAIGCLETVGEKQO--EHEVQWLREHLAML 168
DB 206 HKCVQTLRLSELSELSAHLSECVNAPSTCSFKRYGCV--FOGTNQOIKAEASAVQHVNL 263
QY 169 --LSSVLEAKPLLDGQSHAGSELLQRCESLEKTA--TFENIVCVLNREVER-----216
DB 264 KEWNSLEKK-----VSLQN-ESVEKNKSIQSLHNQICSEFEIERQKEMLRNN 312
QY 217 -----VAMTAEACS-----RQRLDQD-----KIEALSSKVOOLE-----246
DB 313 ESKILHQRVIDSQAEKLEKELDKIRPFQCNWEADSMKSSVESLQNRVTELESVDKSG 372
QY 247 ---RSIGL-----KDLAVADLEQKVLMEASTYDGVFIWKISDFARKLQEA 289
DB 373 QVARNTGLLESQSLRHDQMLSVHDIRLADMDLRFQVLETASYNGVLWIKIRDYKRRKQEA 432
QY 290 VAGRIPAIFSPAYTSRYGYKMCRLIYNGDGTGRGTHLSLFFVVMGPNDAALLRPFNQ 349
DB 433 VMGKTLISYQFFYTGFGYKMCARVYLNGDGMKGTHLSLFFVIMRGYDALLPWPFKQ 492
QY 350 KVTMLLDQ--NNREHVIDAFRDPVTSSTSPQFVNDMNIAAGCPLFCFVSKMAKNSYVRD 408
DB 493 KVTMLMDQSSRRHLGDAFKDPDNSSSFKPTGEMNIAAGCPVFAQTGLE-NGYIKD 551
QY 409 DAIFIKAIVDTGL 422
DB 552 DTIFKIVDTSGL 565

RESULT 12

US-10-242-212-7
; Sequence 7, Application US/10242212
; Publication No. US2003009644A1
; GENERAL INFORMATION:
; APPLICANT: AHUJA, SEENA
; APPLICANT: BONEWALD, LYNDIA
; TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 4003.001000
; CURRENT APPLICATION NUMBER: US/10/242.212
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US/09/645,926
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-212-7

Query Match 32.1%; Score 710; DB 14; Length 567;
Best Local Similarity 32.7%; Pred. No. 5.1e-54;
Matches 181; Conservative 74; Mismatches 128; Indels 170; Gaps 21;

QY 16 QGFSKTLTGKLEAKYLCSACNVLRPFOACQCHRYCSFCLASILSSGPONCAACVHE 75
DB 36 QGGYKEKFKVT-VEKYKCEKCHLVLCSPKQTECHRFCECMAALLSSSPKCTAC-QE 93
QY 76 GIYEGISILESSAPPDNAARREVESLPAVC--PSDGT-----113
DB 94 SIVKDKV-----FKDNCKREILALQIYCRNESRGCAEQMLGLHLVHLKNDCHFEEL 145
QY 114 -----WKGTLKEYEFQDHVK-----TCGKCR--VP-----136
DB 146 PCVRPDCKEKVLKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDPCVVVSCP 205
QY 137 -----CRFHAIGCLETVGEKQO--EHEVQWLREHLAML- 168
DB 206 KCVQTLRLSELSELSAHLSECVNAPSTCSFKRYGCV--FOGTNQOIKAEASAVQHVNL 263
QY 169 --LSSVLEAKPLLDGQSHAGSELLQRCESLEKTA--TFENIVCVLNREVER-----216
DB 264 EWSNSLEKK-----VSLQN-ESVEKNKSIQSLHNQICSEFEIERQKEMLRNE 312
QY 217 -----VAMTAEACS-----RQRLDQD-----KIEALSSKVOOLE-----246
DB 313 SKILHQRVIDSQAEKLEKELDKIRPFQCNWEADSMKSSVESLQNRVTELESVDKSG 372
QY 247 ---RSIGL-----KDLAVADLEQKVLMEASTYDGVFIWKISDFARKLQEA 290
DB 373 VARNTGLESQSLRHDQMLSVHDIRLADMDLRFQVLETASYNGVLWIKIRDYKRRKQEA 432
QY 291 AGRIPALFSPAYTSRYGYKMCRLIYNGDGTGRGTHLSLFFVVMGPNDAALLRPFNQ 350
DB 433 MGKTLISYQFFYTGFGYKMCARVYLNGDGMKGTHLSLFFVIMRGYDALLPWPFKQ 492
QY 351 VTLMLLDQ--NNREHVIDAFRDPVTSSTSPQFVNDMNIAAGCPLFCFVSKMAKNSYVRD 409
DB 493 VTLMLMDQSSRRHLGDAFKDPDNSSSFKPTGEMNIAAGCPVFAQTGLE-NGYIKD 551
QY 410 AIFIKAIVDTGL 422
DB 552 DTIFKIVDTSGL 564

RESULT 13

US-10-207-655-103
; Sequence 103, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207.655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-103

Query Match 32.1%; Score 710; DB 14; Length 567;
Best Local Similarity 32.7%; Pred. No. 5.1e-54;
Matches 181; Conservative 74; Mismatches 128; Indels 170; Gaps 21;

QY 16 QGFSKTLTGKLEAKYLCSACNVLRPFOACQCHRYCSFCLASILSSGPONCAACVHE 75
DB 36 QGGYKEKFKVT-VEKYKCEKCHLVLCSPKQTECHRFCECMAALLSSSPKCTAC-QE 93
QY 76 GIYEGISILESSAPPDNAARREVESLPAVC--PSDGT-----113
DB 94 SIVKDKV-----FKDNCKREILALQIYCRNESRGCAEQMLGLHLVHLKNDCHFEEL 145
QY 114 -----WKGTLKEYEFQDHVK-----TCGKCR--VP-----136

Db 146 PCVRPCKEVLKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPH 205
QY 137 -----CRFAIGLETVEGEKQ--EHEVQWLRHLAML- 168
Db 206 KCSVQVLLRSLSAHLSECNAPSTCSFKRYGCV--FQGNQOIKAHAEASSAVQVNLK 263
QY 169 -LSSVLEAKPLLDQSHAGSELQRCESLEKTA--TFENIVCVLNREVER----- 216
Db 264 EWSNSLEKK-----VSLQON-ESVEKNKSIQSLHNQICSPFEIETQKEMLRNNE 312
QY 217 -----VAMTAERACS-----RQRLDOD-----KIEALSKVQOOLE----- 246
Db 313 SKILHLQRLVIDSOAEKLKELDKERIPRONWEADSMKSSVESLQNRVTELESVDKSAQ 372
QY 247 --RSIGL-----KDLAMADLEQKYLEMEASTYDGVFTWKISDFARKQEAR 290
Db 373 VARTGULSLSRHPDQMSVDIRLADMDLGFQVLETASYNGVLWIKIRDYKRRKQEAR 432
QY 291 AGRIPAFSPFTSYRYGYMCLIRIYINGDGTGRGTHLSLFFVVMKGPNDALLRWPFNOK 350
Db 433 MGKTLSTJSPFFYTGFGYMKCARVYINGDMGKGTHTLSLFFVIMRGEYDALLPWPFOK 492
QY 351 VTMLMLDQ--NNREHVIDAFEPDVTSSSFPVNDNMNIASGCLFCFVSKMEAKNSVYRDD 409
Db 493 VTMLMDQSSRRHLGDAPDPDNSSSFKRPTGEMNIASGCPVFVAQTVLE-NGTYIKDD 551
QY 410 AIFKAIVDLTGL 422
Db 552 TFIKIVDTSGL 564

RESULT 14

US-10-042-865-163
; Sequence 163, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangoli, Bsha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rotherberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: Macdougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09

; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-865-163
Query Match 31.1%; Score 687.5; DB 15; Length 538;
Best Local Similarity 30.2%; Pred. No. 4.7e-52;
Matches 160; Conservative 85; Mismatches 139; Indels 145; Gaps 12;
QY 27 KLEAKYLCSACRNVLRPFPQACGHRYSFCPLASI--LSSGPQNCAACVHEGIEGISI 84
Db 19 RLEERYKCAFCCHSVLHNPHTGCGHRFCQHCILSLRELNTVP-----ICPVDKEV 68
QY 85 LESSAPPDNAAREVSLPAVCP--SDGCTWKGTLKEYEFQDHVYKC-----CKCR 134
Db 69 IKSOEVFKDNCKCKREVLNLVYVYCNAPCNAKVLGRY--QDHLQOCLFQPVQCSNEKR 126
QY 135 VP-----KATTFENIVCVLNREVERVA----- 136
Db 127 EPVLRKDLKEHLSASCQFRKEKCLYCKDVVIVNLQNHENLCPEYFVFCNNCAKILK 186
QY 137 -----CRFAIGLETVEGEKQOEHEVQWLRHLAMLSSVLEAKPLG 180
Db 187 TEVDEHLAVCPAEQDCPFKHYGCAVTDKRNLCQOEHSEHSALREHMLVLEKNVQLEEQIS 246
QY 181 D---QSHAGSELLQRCESLEK-----KTATFENIVCVLNREVERVA----- 218
Db 247 DLHKSLEQESKIQOQLAETIKLEKEKQFAQLFGKNGSLPNIQVFASHIDKSANLEAQ 306
QY 219 ---MTAEACSRQRLD---QDKIEALSSKVQOOLERS-----IGLKD 254
Db 307 VHQLLMVNVQOONKFDLRPLMEAVDTVKQKITLLENDDQRLAVLEETNKHDTHINHA 366
QY 255 AMADLEQKYLEMEASTYDGVFIKISDPARKLOBAVAGRIPAEPAFTSYRYGYMCLIR 314
Db 367 QLSXNEERFKULEGTCTYNGKLIWKVTDYKMKRRAVDGHTVSIQSFYTSRCGYRJCAR 426
QY 315 IYLMGDTGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDQNNREHVIDAFRDPVTS 374
Db 427 AYLMGDSGSGSHLSLYFVVMRGEFDSLLQWFFRQVTLMLDQSGKKNIMETFKPDPS 486
QY 375 SSFQRPVNDNMNIASGCLFCFVSKME-AKNSVYRDDAIFKAIYDLTGL 422
Db 487 SSFKRPDGMNIASGCPRFVAHSLVLENKAKYIKDDTLFLKVAVDLTL 535

RESULT 15

US-10-004-378A-34
; Sequence 34, Application US/10004378A
; Publication No. US20030228301A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Furtak, Kazaryna
; APPLICANT: Perna, Amanda
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkuts, Richard A
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Casman, Stacie J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Vernet, Corrine A

Query Match	31.1%	Score	687.5;	DB	14;	Length	557;
Best Local Similarity	30.2%;	Midg. No.	4.9e-52;				
Matches	160;	Conservative	85;	Mismatches	139;	Indels	145;
Gaps	12;						
QY	27	KLEAKYLCACRNVLRRPFOAQCGHRYCSFCGLASI--LSSGPONCAACVHEGIYEEGISI	84				
DB	38	RLEERYKACFCHSVLHNPHQTGCGHRCFQCHILSLRELNTVP-----ICPVDKEV	87				
QY	85	LESSASFPDNNARREVESLPAVCP-SDGCTWGTGTLKEYEFQDHVTC-----GKCR	134				
DB	88	IKSOEVFKDNCCKREVLNLVYVCSNAPGCKNAKVLGRY-QDHQQCLFPQVQCSNEKCR	145				
QY	135	VP-----	136				
DB	146	EPVLRKDLKHELSASCQFRXCKCLYCKDWWINLQNHEENLCPEYPVFCPNNCAKIILK	205				
QY	137	-----CRFHAICGLTVEGGEKQOEHVQWLREHLAMLSSVLEAKPLLG	180				
DB	206	TEVDEHLAVCPAEAQDCPFKHYGCATYDKRNLQOEHSAURHEHRLVLEKQVLEQSIS	265				
QY	181	D-----QSHAGSELLQRCSELEK-----KTATFENIVCVLNRREYVA-----	218				
DB	266	DLHLSLEKQSKSKIQLAATTIKLEKEFKOPALFGNGSFPNTIOVFASHIDKSAWLEAQ	325				

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2004, 16:19:28 ; Search time 39 Seconds
(without alignments)
1041.115 Million cell updates/sec

Title: US-10-018-030B-2

Perfect score: 2211

Sequence: 1 MAAASVTPGSLLELQPGFS.....NSVVRDAIFKAIYDLTGL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

P1R_79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2156.5	97.5	501	2 S56163	tumor necrosis fac
2	1914.5	86.6	501	2 I61512	TNF receptor assoc
3	733.5	33.2	416	2 B55649	TNFR-associated pr
4	730	33.0	567	2 I49272	CD40 receptor-asso
5	727	32.9	409	2 A54750	TNF receptor assoc
6	722	32.7	543	2 S68467	CD40 receptor-asso
7	717.5	32.5	568	2 A55360	tumor necrosis fac
8	687.5	31.1	557	2 JC6539	MLN 62 protein - h
9	496	22.4	470	2 I38026	probable interleuk
10	408	18.5	522	2 S71821	hypothetical prote
11	395	17.9	509	2 T22338	endopeptidase 2 (E
12	139	6.3	748	2 S24334	neprin A (EC 3.4.2
13	135	6.1	704	2 A48040	recombination acti
14	133.5	6.0	1073	2 I51055	neprin A (EC 3.4.2
15	132.5	6.0	668	1 A42908	neprin A (EC 3.4.2
16	131	5.9	746	1 HYHUMA	neprin A (EC 3.4.2
17	124	5.6	760	2 A40195	probable zinc-bind
18	123.5	5.6	624	2 S28418	transcription regu
19	123	5.6	442	2 A57041	ring finger B-box
20	122	5.5	638	2 JC7753	neprin A (EC 3.4.2
21	122	5.5	700	1 HYHUMB	kinesin-related pr
22	121	5.5	2954	2 T14156	RING finger protei
23	119.5	5.4	506	2 S37583	recombination-acti
24	118	5.3	1043	2 B33754	testis-abundant fi
25	115.5	5.2	518	2 JC7387	hypothetical prote
26	115	5.2	944	2 T28734	transforming prote
27	114	5.2	801	4 TVHURE	ret finger protein
28	113.5	5.1	513	1 TVHURF	PML-1 protein - hu
29	113.5	5.1	560	2 A40044	

RESULT 1

S56163

tumor necrosis factor type 2 receptor associated protein - human

N:Alternate names: TNF receptor-associated protein

C:Species: Homo sapiens (man)

C>Date: 10-Oct-1995 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004

C:Accession: S56163; S58925; S58926; I38729

R:Song, H.Y.; Donner, D.B.

Biochem. J. 309, 825-829, 1995

A:Title: Association of a RING finger protein with the cytoplasmic domain of the human t

A:Reference number: S56163; MUID:95366958; PMID:7639698

A:Accession: S56163

A:Molecule type: mRNA

A:Residues: 1-501 <SON1>

A:Cross-references: UNIPROT:Q12933; EMBL:U12597; NID:975272

R:Song, H.Y.; Donner, D.

submitted to the EMBL Data Library, July 1994

A:Description: Association of a RING finger protein with the cytoplasmic domain of the h

A:Reference number: S58925

A:Accession: S58925

A:Molecule type: mRNA

A:Residues: 1-42,63-342,363-501 <SON2>

A:Cross-references: EMBL:U12597; NID:975272

A:Accession: S58926

A:Molecule type: mRNA

A:Residues: 1-342,'RPPQACGHRYSFCLASIL',363-501 <SON3>

A:Cross-references: EMBL:U12597; NID:975272; PIDN:AAAS7706.1; PID:975273

R:Roche, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.

Cell 78, 681-692, 1994

A:Title: A novel family of putative signal transducers associated with the cytoplasmic do

A:Reference number: A54750; MUID:94349371; PMID:8069916

A:Accession: I38729

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-342,'RPPQACGHRYSFCLASIL',363-501 <ROT>

A:Cross-references: EMBL:U12597; NID:975272; PIDN:AAAS7706.1; PID:975273

C:Genetics:

A:Gene: GDB:TRAF2; TRAF

A:Cross-references: GDB:6268629; OMIM:601895

A:Map position: 9q34-q34

C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology

C:Keywords: zinc finger

F:30-78/Domain: RING finger homology <RNG>

Query Match 97.5%; Score 2156.5; DB 2; Length 501;

Best Local Similarity 84.0%; Pred. No. 3.5e-151;

Matches 421; Conservative 0; Mismatches 1; Indels 79; Gaps 1;

OY 1 MAAASVTPGSLLELQPGFSKTLTGKLEAKYLCSACNVLRPPQACGHRYSFCLAS 60

DB 1 MAAASVTPGSLLELQPGFSKTLTGKLEAKYLCSACNVLRPPQACGHRYSFCLAS 60

QY 61 ILSSGPQCAACVHGIYEEGIISSLESSAPPDNAAREVESLPAVCPSDCTWKGLKE 120
 Db |||||
 QY 61 ILSSGPQCAACVHGIYEEGIISSLESSAPPDNAAREVESLPAVCPSDCTWKGLKE 120
 Db |||||
 QY 121 YE----- 122
 Db ||
 QY 121 YESCHEGRCLMLTECPACKGLVRLGEXERHLEHPCPERSLSCHRCRAPCCGADVKAHHE 180
 Db ||
 QY 123 ----- 122
 Db ||
 QY 181 VCPKPLFLDCGKKKIPREFQDHVTCGKRCVPCRFHAIGCLTVEGEKQHEVQWL 161
 Db |||||
 QY 162 REHLAMLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVANTA 221
 Db |||||
 QY 241 REHLAMLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVANTA 300
 Db |||||
 QY 222 EACSRQHLDDQKIBALSSKVQOLERSIGLKDLMADLEQKLEMEASTYDGVFIWKISD 281
 Db |||||
 QY 301 EACSRQHLDDQKIBALSSKVQOLERSIGLKDLMADLEQKLEMEASTYDGVFIWKISD 360
 Db |||||
 QY 282 FARKLOEAVAGRIPAIFSPAFYTSRYGKMCRLRYLNGDGTGRGTHLSLFFVVMKGPND 341
 Db |||||
 QY 361 FPKLOEAVAGRIPAIFSPAFYTSRYGKMCRLRYLNGDGTGRGTHLSLFFVVMKGPND 420
 Db |||||
 QY 342 LLRWFNFQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVNDMNIAAGCPLFCPVSKWEA 401
 Db |||||
 QY 421 LLRWFNFQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVNDMNIAAGCPLFCPVSKWEA 480
 Db |||||
 QY 402 KNSYVRDDAIFKAIVDLTGL 422
 Db |||||
 QY 481 KNSYVRDDAIFKAIVDLTGL 501
 Db |||||
 RESULT 2
 I61512
 TNF receptor associated factor 2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I61512
 R:Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
 Cell 78, 681-692, 1994
 A:Title: A novel family of putative signal transducers associated with the cytoplasmic
 A:Reference number: A54750; MUID:94349371; PMID:8069916
 A:Accession: I61512
 A>Status: preliminary; translated from GS/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-501 <RES>
 A:Cross-references: UNIPROT:P39429; GB:L35303; NID:G532620; PIDN:AAC37662.1; PID:G532621
 C:Genetics:
 A:Gene: TRAF2
 C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 C:Keywords: zinc
 F:30-78/Domain: RING finger homology <RNG>
 Query Match 86.6%; Score 1914.5; DB 2; Length 501;
 Best Local Similarity 74.3%; Pred. No. 2.4e-133;
 Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;
 QY 1 MAASVTPPGSLELLQPGFSKTLGLTKLEAKYLCACRNVLRRFPQACGHRVCSFCLAS 60
 Db |||||
 QY 1 MAASVTPPGSLELLQPGFSKTLGLTKLEAKYLCACRNVLRRFPQACGHRVCSFCLAS 60
 Db |||||
 QY 61 ILSSGPQCAACVHGIYEEGIISSLESSAPPDNAAREVESLPAVCPSDCTWKGLKE 120
 Db |||||
 QY 61 ILSSGPQCAACVHGIYEEGIISSLESSAPPDNAAREVESLPAVCPSDCTWKGLKE 120
 Db |||||
 QY 121 YE----- 122
 Db ||
 QY 121 YESCHEGLCPFLTECPACKGLVRLSEKHTEQECPKRSLSQCHRCRAPCSHVDLVHVE 180
 Db |||||
 QY 123 ----- 122
 Db ||
 QY 181 VCPKPLFLDCGKKKIPREFQDHVTCGKRCVPCRFHAIGCLTVEGEKQHEVQWL 161
 Db |||||
 QY 181 VCPKPLFLDCGKKKIPREFQDHVTCGKRCVPCRFHAIGCLTVEGEKQHEVQWL 240
 Db |||||

QY 162 REHLAMLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVANTA 221
 Db |||||
 QY 241 REHLAMLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVANTA 300
 Db |||||
 QY 222 EACSRQHLDDQKIBALSSKVQOLERSIGLKDLMADLEQKLEMEASTYDGVFIWKISD 281
 Db |||||
 QY 301 EACSRQHLDDQKIBALSSKVQOLERSIGLKDLMADLEQKLEMEASTYDGVFIWKISD 360
 Db |||||
 QY 282 FARKLOEAVAGRIPAIFSPAFYTSRYGKMCRLRYLNGDGTGRGTHLSLFFVVMKGPND 341
 Db |||||
 QY 361 FTKROEAVAGRIPAIFSPAFYTSRYGKMCRLRYLNGDGTGRGTHLSLFFVVMKGPND 420
 Db |||||
 QY 342 LLRWFNFQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVNDMNIAAGCPLFCPVSKWEA 401
 Db |||||
 QY 421 LLRWFNFQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVNDMNIAAGCPLFCPVSKWEA 480
 Db |||||
 QY 402 KNSYVRDDAIFKAIVDLTGL 422
 Db |||||
 QY 481 KNSYVRDDAIFKAIVDLTGL 501
 Db |||||
 RESULT 3
 B55649
 TNFR-associated protein EB16 - human
 C:Species: Homo sapiens (man)
 C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C:Accession: B55649
 R:Nosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E.
 Cell 80, 389-399, 1995
 A:Title: The Epstein-Barr virus transforming protein LMPI engages signaling proteins for
 A:Reference number: A55649; MUID:95163092; PMID:7859281
 A:Accession: B55649
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-416 <MOS>
 A:Cross-references: UNIPROT:Q13077; GB:U19261; NID:9675461; PIDN:AAA62309.1; PID:9675462
 Query Match 33.2%; Score 733.5; DB 2; Length 416;
 Best Local Similarity 37.8%; Pred. No. 1.8e-46;
 Matches 156; Conservative 65; Mismatches 109; Indels 83; Gaps 6;
 QY 55 SFCLASILSSGPQ-----CAACVHGIYEEGIISSLESSAPPDNAAREVESLPAVCPS 109
 Db |||||
 QY 35 ALCCAGCUSENPRNGEDQICPKRGEDL-----QSISPGSRLRQSKAHPEV--- 81
 Db |||||
 QY 110 DGGTCKGTLKEYEQDHVTCGKRCVPCRFHAIGCLTVEGEKQHEVQWLREHLAML 169
 Db |||||
 QY 82 -----AEACIGCPFAGVCGSPKSPQSVQHEVTSQTSHLNLL 120
 Db |||||
 QY 170 SSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVANTA 180
 Db |||||
 QY 121 GFMQKWKARLGGLESFMALEQNLSDLQQAEEVAGDLEVDVCYRAPCSSESQEEALQ 180
 Db |||||
 QY 195 -----SLEKKTATFENIVCVLNREVERVANTAACSRQHLDDQKIBALSSKVQOL 246
 Db |||||
 QY 181 FMKEKLLAELEKLRVFNIVAVLNKEVEASHALATSIHQSLDREILSLEQEVVLO 240
 Db |||||
 QY 247 RSIGLKDLMADLEQKLEMEASTYDGVFIWKISDPARKLOEAVAGRIPAIFSPAFYTSR 306
 Db |||||
 QY 241 QTLAQDQALGKLEQSLRMBEASPDGTFLWKITNVTTRCHESACGRTVSLFSPAFYAK 300
 Db |||||
 QY 307 YGYKMCRLRYLNGDGTGRGTHLSLFFVVMKGPNDALRWPENQKVTMLLDQNNREHVID 366
 Db |||||
 QY 301 YGYKMCRLRYLNGDGTGRGTHLSLFFVVMKGPNDALRWPENQKVTMLLDQNNREHVID 360
 Db |||||
 QY 367 AFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKWEA-KNSYVRDDAIFKAIVD 418
 Db |||||
 QY 361 AFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKWEA-KNSYVRDDAIFKAIVD 418
 Db |||||
 RESULT 4
 I49272

CD40 receptor-associated factor 1 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
 C/Accession: I49272
 R/Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
 Science 267, 1494-1498, 1995
 A/Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
 A/Reference number: A55960; MUID:95184010; PMID:7533327
 A/Accession: I49272
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-567 <RES>
 A/Cross-references: UNIPROT:Q60803; EMBL:U21050; NID:g719292; PIDN:AAC52175.1; PID:g719292
 C/Genetics:
 A/Gene: CRAF1
 C/Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 C/Keywords: zinc finger
 F/48-96/Domain: RING finger homology <RNG>

Query Match 33.0%; Score 730; DB 2; Length 567;
 Best Local Similarity 32.1%; Pred. No. 4.9e-46;
 Matches 187; Conservative 80; Mismatches 131; Indels 184; Gaps 22;

QY 1 MAAASVTPPGSLLOP-----GFSKTLTGKLEAKYLCACRVLRPFOA 47
 DB 7 MDAAGTLQNPPLKLPDRGAGSVLPVPEQGYKEKFKVT-VEKDYKCEKRLVLCNPKQT 65
 QY 48 QCHRRVCSFCLASILSGPQNCACVHGIEYERGISILESSAAPPDPAARVESLPVAVC 107
 DB 66 ECGHRCFCSMAALLSSSPKCTAC-CESEIHKDV-----FDNCCRBILALQVYC 116
 QY 108 PSD-GCTWKGTL-----KEYEFO-----DHYK-----TC 130
 DB 117 RNSGRCAEGLTGLHLLVHLKNCQFELPLRADCKEVLKDLRDHVEKACKYREATC 176
 QY 131 GKCR--VP-----D-----CRPHAI 142
 DB 177 SHCKSQVPMIKLOKHEDTDCPVVSCPHKCSQVTLRLSELSAHLSECVNAPSTCSFKY 236
 QY 143 GCLTEVEGEKQ--EHEVQVLRHLAML--LSSVLEAKPLGQSHAGSELLQRCSELEK 198
 DB 237 GCY--FGQTNQOIKAEHASSAVOHVLLKWSNLEKK-----VSLIQN-ESVEK 283
 QY 199 KTA--TFENIVCVLNREVER-----VAMTAEACS-----RQHR 229
 DB 284 NKSIQSLHNOICFETIEIEROKEMLRNNEKILHLQKVIDSQAEKLKELDKRIPRQXW 343
 QY 230 LDQP-----KLEALSSKVOOLE-----RSIGLKDLAMADLEQ 261
 DB 344 EADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQLSRHDQTLVSHDIRLADMDL 403
 QY 262 KVLEMEASTYDGVFIWKISDFARKLOFAVAGRIPAIFSPAFYTSRYGYKNCRLIYILNGDG 321
 DB 404 RFQVLETASVNGVLIWKIRDYKRRKQEAVMGKTLISLYSQPFYTGFGYKWCARVYLNGDG 463
 QY 322 TGRGTHLSLFPVVMKGNDAKLRPNQKVTMLLDQ--NNREHVIDAFRDPVTSSSFQRP 380
 DB 464 MGKGTHTLSLFPVIMRGEDYDALLPWPFKQKVTMLMDQSGSSRRHLGDAFRDPDNSSSFQRP 523
 QY 381 VNDNNIASGCPFCVPSKMKAKNSYVRDDAIFIKAVDITGL 422
 DB 524 TGMENIASGCPVFAQTIVLE-NGTYIKDDTIFIKVIVDSIDL 564

RESULT 5
 A54750
 TNF receptor associated factor 1 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: A54750
 R/Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
 Cell 78, 661-692, 1994
 A/Title: A novel family of putative signal transducers associated with the cytoplasmic d

A/Reference number: A54750; MUID:94349371; PMID:8059916
 A/Accession: A54750
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-409 <RES>
 A/Cross-references: UNIPROT:P39428; GB:L35302; NID:g532618; PIDN:AAC37663.1; PID:g532619
 C/Genetics:
 A/Gene: TRAF1

Query Match 32.9%; Score 727; DB 2; Length 409;
 Best Local Similarity 38.5%; Pred. No. 5.4e-46;
 Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;

QY 85 LESSAPFDNAAARVESLPAVCSDG---CTWKGTLKEYEFODHVKYTKGKCR----- 134
 DB 1 MASSAPDENEFQGCPPAPQDPSEPRVLCCT--ACLSNLRDDEDRICPKCRADNLHP 58
 QY 135 -----VPCRFAIGCLTVEGEKQKEHEVQWLRHLAMLSSVLE 174
 DB 59 VSPGSLTQEKVHSDVAEAEIMCPFAGVGCFSKSPQSMQHEATSSSHLYLLAVLKE 118
 QY 175 AKPLLDGSHAGSLLQR-----CES----- 195
 DB 119 WKSPPGSLNLSAPALERNLSELOQAAVEATGDLVDVCRAPCCESQEEALQHLVKEK 178
 QY 196 ---LEKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVOQLERSIGL 251
 DB 179 LLAQLEELKRVFANIVAVLNKEVEASHLALAASHQSLDREHLLSLQEVVELOQILAQ 238
 QY 252 KDLAMADLEQKVLMEASTYDGVFIWKISDFARKLOFAVAGRIPAIFSPARYTSRYGYK 311
 DB 239 KDQVLGKLEHSLRLMEBASFDGTFLWKITNTVKRCHESVCGRTVSLFSPAFYTKYGYKL 298
 QY 312 CLRIYLNCDGGRGTHLSLFPVVMKGNDAKLRPNQKVTMLLDQNNRHSHVDAFRPD 371
 DB 299 CLRIYLNCDGGRGTHLSLFPVIMRGEDYDALLPFPFNKVTFMLLDQNNREHDAFRPD 358
 QY 372 VTSSSFQRPVNDNNIASGCPFCVPSKMEAA-KNSYVRDDAIFIKAVD 418
 DB 359 LSSASFQRPQSETNVASGCPFLFFPLSKLQSPKHAYVKDDTMFLKCIVD 406

RESULT 6
 S68467
 CD40 receptor-associated protein CAP-1 - human
 C/Species: Homo sapiens (man)
 C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C/Accession: S68467; I53498
 R/Sato, T.; Irie, S.; Reed, J.C.
 FEBS Lett. 358, 113-118, 1995
 A/Title: A novel member of the TRAF family of putative signal transducing proteins binds
 A/Reference number: I53498; MUID:95129692; PMID:7530216
 A/Accession: S68467
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-343 <SAL>
 A/Cross-references: UNIPROT:Q13114; EMBL:L38509; NID:g695357; PIDN:AAA68195.1; PID:g695357
 A/Experimental source: tissue-type fetal brain
 C/Genetics:
 A/Gene: CAP-1
 C/Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 C/Keywords: homodimer; signal transduction; zinc finger
 F/49-97/Domain: RING finger homology <RNG>

Query Match 32.7%; Score 722; DB 2; Length 543;
 Best Local Similarity 34.9%; Pred. No. 1.8e-45;
 Matches 184; Conservative 77; Mismatches 124; Indels 142; Gaps 23;

QY 16 QGFPSKTLTGKLEAKYLCACRVLRPFOAQCHRYCSFCLASILSSGQNCACVHE 75
 DB 36 QGGYKEKFKVT-VEKDYKCEKCHLVLCSPKQTEGCRFCSCMAALLSSSPKCTAC-QE 93
 QY 76 GIYERGISILESSAAPPDPAARVESLPVAVC--PSDGTWKGTL----- 118

Db 94 SIVKDV-----FKNCCKREILALQIYCRNESRGCAEQTLGLHLLVHLKNDCHFEE 145
 QY 119 -----KE-----YEFQDHVK-----TCGKCR--VP-----CRFHAGC- 144
 Db 146 LPCVRPDCCKEVLRLDRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCP 205
 QY 145 ----LETV-----EGEKQO--EHEVQMLREHLAML--LSSVLEAKPLLGQSHAGSELLQRC 193
 Db 206 HKCSVQTLRLRSGTNOQIKAHASAVQHVNLKREWSNLEKK-----VSLQON- 254
 QY 194 ESELEKTTA--TFENIVCVLNREVER-----VAMTAEACS----- 225
 Db 255 ESVEKNKTSQSLHNOICFSFEIERQKEMLRNNEKILHLQVRIDQAEKLEKLDKEIRS 314
 QY 226 -RQHLDDO---KTEALSSKVOOLE-----RSIGL-----KDLAM 256
 Db 315 FRQWEEADSMKSSVESLQNRVTELESVDKSGAQVARTGLESQLSRHDQMLSVHDIRL 374
 QY 257 ADLEQKVLMEASTYDGVFIWKISDFARKLQEAQVAGRIAPAFISPAFYTSRYGYKMCRLIY 316
 Db 375 ADMDLRFQVLETASVNGVLIWKIRYKRRKQEAQVNGKTLISYQPFYTGFGYKMCARVY 434
 QY 317 LNCDCGTGTHLSLFFVVMKGNDAALLRPKNOKVTLMLDDO--NNREHVIDAFEPDYTSS 375
 Db 435 LNDGNGKGTLSLFFVIMRGEDYDALLPWPFPKQVTLMLDQGSRRHLGDAFKPDNNS 494
 QY 376 SFQRPVNDMNIAAGCPFLCPVSKMEAKNSYVRDDAIFIKAIYDVTGL 422
 Db 495 SFPKPTGEMNIAAGCPVFEVQATVLE-NGTYIKDDTIFIKIVDTSDL 540

RESULT 7
 A:55960
 CD40 receptor-associated factor 1 - human
 N:Alternate names: CD40-binding protein
 C:Species: Homo sapiens (man)
 C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
 C:Accession: A55960; A55135
 R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D. Science 267, 1494-1498, 1995
 A:Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
 A:Reference number: A55960; MUID:95184010; PMID:753327
 A:Accession: A55960
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-568 <RES>
 A:Cross-references: UNIPROT:Q13114; EMBL:U21092; NID:G726087; PIDN:AA50112.1; PID:G7260
 R:Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E. Cell 80, 389-399, 1995
 A:Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for
 A:Reference number: A55649; MUID:95163092; PMID:7859281
 A:Accession: A55649
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-128, 'M', 130-568 <MOS>
 A:Cross-references: GB:U19260; NID:G675459; PIDN:AAA65732.1; PID:G675460
 R:Hu, H.M.; O'Rourke, K.; Bonuski, M.S.; Dixit, V.M. J. Biol. Chem. 269, 30069-30072, 1994
 A:Title: A novel RING finger protein interacts with the cytoplasmic domain of CD40.
 A:Reference number: A55135; MUID:95073988; PMID:7527023
 A:Accession: A55135
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-128, 'M', 130-133, 135-404, 'G', 406-568 <HUA>
 A:Cross-references: GB:U15637; NID:G595910; PIDN:AAA56753.1; PID:G595911
 C:Genetics:
 A:Gene: CRAF1
 C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 C:Keywords: coiled coil; zinc
 F:49-97/Domain: RING finger homology <RNG>

Query Match 32.5%; Score 717.5; DB 2; Length 568;
 Db

Best Local Similarity 33.2%; Pred. No. 4.1e-45;
 Matches 184; Conservative 75; Mismatches 124; Indels 171; Gaps 22;

QY 16 QPQFSKTLTGKLEAKYLCACRNVLRRPFOACQGHRYCSFCLASILSSGPQNCACVHE 75
 Db 36 QGQYKFKVKT-VEQYKCEKCHLVLCSPKQTECHGRFCESCMAALLSSSPFKTAC-QE 93
 QY 76 GIYEEGISILESSAPPDAAARVESLPAVC--PSDGGCTWKGTL----- 118
 Db 94 SIVKDV-----FKNCCKREILALQIYCRNESRGCAEQTLGLHLLVHLKNDCHFEE 145
 QY 119 -----KE-----YEFQDHVK-----TCGKCR--VP----- 136
 Db 146 LPCVRPDCCKEVLRLDRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCP 205
 QY 137 -----HKCSVQTLRLRSELASHLSECVNAPSTCSFKRYGCV--FOGTNQOIKAHASAVQHVNL 263
 Db 206 HKCSVQTLRLRSELASHLSECVNAPSTCSFKRYGCV--FOGTNQOIKAHASAVQHVNL 263
 QY 169 --LSSVLEAKPLLGQSHAGSELLQRCSELEKTTA--TFENIVCVLNREVER----- 216
 Db 264 KEWSNLSLEKK-----VSLQON-ESVEKNKTSQSLHNOICFSFEIERQKEMLRNN 312
 QY 217 -----VAMTAEACS-----RQHLDDO-----KTEALSSKVOOLE----- 246
 Db 313 ESKILHLQVRIDQAEKLEKLDKEIRPFRQWEEADSMKSSVESLQNRVTELESVDKSGAG 372
 QY 247 ---RSIGL-----KDLAMADLEQKVLMEASTYDGVFIWKISDFARKLQEA 289
 Db 373 QVARTNGLESQLSRHDQMLSVHDIRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEA 432
 QY 290 VAGRIAPAFISPAFYTSRYGYKMCRLIYNGDGTGTHLSLFFVVMKGNDAALLRPKNQ 349
 Db 433 VMGKTLISYQPFYTGFGYKMCARVYNGDGMGKGTLSLFFVIMRGEDYDALLPWPFPKQ 492
 QY 350 KVTMLDDO--NNREHVIDAFRPDVTSSGFORPVNDMNIAAGCPFLCPVSKMEAKNSYVRD 408
 Db 493 KVTMLMDQGSRRHLGDAFKPDNNSFKKPTGEMNIAAGCPVFEVQATVLE-NGTYIKD 551
 QY 409 DAIFIKAIYDVTGL 422
 Db 552 DTIFIKIVDTSDL 565

RESULT 8
 JC6539
 tumor necrosis factor receptor-associated factor 5 homolog - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C:Accession: JC6539
 R:Mizushima, S.; Fujita, M.; Ishida, T.; Azuma, S.; Kato, K.; Hirai, M.; Yama Gene 207, 135-140, 1998
 A:Title: Cloning and characterization of a cDNA encoding the human homolog of tumor necr
 A:Reference number: JC6539; MUID:98172745; PMID:9511754
 A:Accession: JC6539
 A:Molecule type: mRNA
 A:Residues: 1-557 <MIZ>
 A:Cross-references: UNIPROT:Q00463; DDBJ:AB000509; NID:G2982670; PIDN:BAA25262.1; PID:G2
 C:Comment: This protein is involved in transduction of signals from various tumor necrosi
 mphtoxin-beta receptor.
 C:Genetics:
 A:Map position: 1q32.3-1q41.1
 C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 C:Keywords: coiled coil; tumor; zinc finger
 F:41-90/Domain: RING finger homology <RNN>

Query Match 31.1%; Score 687.5; DB 2; Length 557;
 Best Local Similarity 30.2%; Pred. No. 6.4e-43;
 Matches 160; Conservative 85; Mismatches 139; Indels 145; Gaps 12;

QY 27 KLEAKYLCACRNVLRRPFOACQGHRYCSFCLASI--LSSGPQNCACVHEGIYEEGISI 84
 Db 38 RLEERYKCAFCHSVLHNPHQTCCGHRFCQHCILSRELNTVP-----ICPVDREV 87

Db 233 LDCPTAPICTESTFGCEKMKQNRHLARHQENTQSHRMLAQPV-HSLSVIPDSGYI-- 289
QY 188 ELLQRCESLEKKTATFENIVCLAREVERVAMTAACSRHRLDQ--DKIALSKVQOL 245
Db 290 -----SEVRNFQETIHOLEGLVR-----ODHOIRELTAKMETQSMYSEL 330
QY 246 ERSIGLKDLAMADLEQKQVLEAEASTYDGVFWIKISDFARKLQEAQVAGRIPAFSPAFVTS 305
Db 331 KRTI-----RTLEDKVAIEAQOCNGIYIKWIGNFGMLKCOEEKPVVHSPGYTG 383
QY 306 RYGYKMCRIYINGDGTGR-GTHLSLFFVVMKGPNDALLRPPFKQKVTMLLDQN----- 359
Db 384 KPGYKLCMLRLHLQLETAQRACANYISLFTMQGEYDSHLPFPFGOTRLTLTDQSEAPVR 443
QY 360 -NREHVIDAFRPDVTSSSFQRPVNDNLAS--GCPFLFCFVSKMEAKNSVVRDDAIFIKAVI 417
Db 444 QNHSEIMDA-KPELL--AFQRTPIRNPFGYVTFMHEALR-ORTFIKDDTLILVRCEV 499

RESULT 11
T22238
hypothetical protein F45G2.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22238
R.Lindsay, S.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19535
A:Accession: T22238
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-509 <WIL>
A:Cross-references: UNIPROT:O62248; EMBL:Z93382; PIDN: CAB07615.1; GSPDB:GN00021; CESP:F4
A:Experimental source: clone F45G2
C:Genetics:
A:Gene: CESP:F45G2.6
A:Map position: 3
A:Introns: 94/2; 119/3; 201/3; 223/3; 249/1; 277/3; 300/3; 327/3; 350/1; 395/3; 448/3
C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
F:161-107/Domain: RING finger homology <RR>

Query Match 17.9%; Score 395; DB 2; Length 509;
Best Local Similarity 26.7%; Pred. No. 2e-21;
Matches 117; Conservative 65; Mismatches 171; Indels 86; Gaps 16;
QY 28 LEAKYLSACRNVLRRPQAOAGHYRSCFLASILSSGPQNCACVHEGYBEGISLES 87
Db 59 LPADCTCPICBQALRDPKLCNDHHYCRQCPEN--ENRTFGCAACQ-----TTIQP 107
QY 88 SSAPFDNAAREVESLPAVC--PSDGCTWKT-----LKEYEFQDHVKTGKC----- 133
Db 108 ELCOHDKAKQKQIALPVCTFESSGCPWDQGLTLDHDLSECTFKSLK-CEKCGEQA 166
QY 134 -----RVPGRFHAIGCTEVEGEKQOEHEVQWLEHRLAVLLSSVLEAKPLL 179
Db 167 KNDLEKHRAKCELARAVGSF---CNKTIKRDREHPKTPQVVIISCPFCQGLTDPRPL 222
QY 180 GDQSHAGSELQRCESLEKKTATFENIVCLNREVERVAMTAACSRHRLDQ----- 232
Db 223 BIEAHCPB-----CPNVD--NVCPVPFGCTTAGKESI-----QQHLSDFPVRHLMY 268
QY 233 ---DKIEALSSKVOQLERSIGLKDLAMADLEQKQVLEAEASTYDGVF-----IKWISDFARKL 286
Db 269 LCDBITDLKGYVELMERDVG---SFNDQRTILS-AAETCTEMFGQLIKWIKIDKLQRT 323
QY 287 QEAVAGRIPAFSPAFVTSRYGYKMCRIYINGDGTGRGTHLSLFFVVMKGPNDALLRWP 346
Db 324 NEAKSGADTTIFSVFVMSHREGYKQMAACFLFGDSAGKSIISLYVLLKGFEDPTLEWP 383
QY 347 FNQKVTMLLDQN-----NREHVIDAFRPDVTSSSFQRPVNDNLASGCPFLFCFVSKM 399
Db 384 FHRAIKISLLDQNPREDRVNITVIDPRKLANEKFLARPGERNAAFSGSFCSLAIL 443

QY 400 EAKNSVVRDDAIFIKAVI 418
Db 444 Q-----NYVKDDKIYQIDVD 459

RESULT 12
S24134
endopeptidase 2 (EC 3.4.24.-) - rat
N:Alternate names: endopeptidase 24.18
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S24134
R:Corbell, D.; Gaudoux, F.; Mainwright, S.; Ingram, J.; Kenny, A.J.; Boileau, G.; Crine, P.EBS Lett. 309, 203-208, 1992
A:Title: Molecular cloning of the alpha-subunit of rat endopeptidase-24.18 (endopeptidase
A:Reference number: S24134; MUID:92371675; PMID:1505684
A:Accession: S24134
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-748 <COR>
A:Cross-references: UNIPROT:O64230; GB:S43408; NID:G254297; PIDN:AAB23030.1; PID:G254298
C:Superfamily: meprin; astacin homology; EGF homology; MAM homology
C:Keywords: hydrolase; metalloproteinase; zinc
F:76-262/Domain: astacin homology <AST>
F:265-434/Domain: MAM homology <MAM>
F:676-711/Domain: EGF homology <EGF>
F:156,160,166/Binding site: zinc (His) #status predicted
F:157/Active site: Glu #status predicted

Query Match 6.3%; Score 139; DB 2; Length 748;
Best Local Similarity 27.0%; Pred. No. 0.023; Mismatches 26; Indels 34; Gaps 8;
Matches 47; Conservative 67;
QY 276 IWKISDFARKLQEAQVAGRIPAFSPAFVTSRYGYKMCRIYINGDGTGRGTHLSLFFVVM 335
Db 436 VMTIRNISQVLENTVKG--DRIVSRPFVNSE-GYGFVTLVPNGRITNSGVGLAFHLY 492
QY 336 KQPNDALEWPF-NOKVTMLLDQ-----NREHVIDAFRPDVTSSSFQ----- 378
Db 493 SGDNVDVILEWPEVEQAINTILDQEPDARNRMSLSMF-----TTSKYQTSSAINGSVIND 548
QY 379 RPVNDNLASGCPFLFCFVTS-----KMEAKNSVVRDDAIFIKAVI 422
Db 549 RTKVGVDYKDCDCFRSIDMGWQALSHQMLRRNFLKDLILIFVDFKDLTHL 602

RESULT 13
A48040
meprin A (EC 3.4.24.18) beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 17-Feb-2003
C:Accession: A48040
R:Gorpea, C.M.; Marchand, P.; Jiang, W.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Bc
J. Biol. Chem. 268, 21035-21043, 1993
A:Title: Cloning, expression, and chromosomal localization of the mouse meprin beta subu
A:Reference number: A48040; MUID:94012651; PMID:8407940
A:Accession: A48040
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-704 <GOR>
A:Cross-references: GB:L15193
C:Superfamily: meprin; astacin homology; EGF homology; MAM homology
C:Keywords: hydrolase; metalloproteinase; zinc
F:72-258/Domain: astacin homology <AST>
F:261-430/Domain: MAM homology <MAM>
F:611-646/Domain: EGF homology <EGF>
F:153,157,163,212/Binding site: zinc (His, His, Tyr) #status predicted
F:154/Active site: Glu #status predicted

Query Match 6.1%; Score 135; DB 2; Length 704;
Best Local Similarity 25.9%; Pred. No. 0.043; Mismatches 35; Indels 40; Gaps 10;
Matches 45; Conservative 35;


```
C>Accession: A42908
R>Johnson, G.D.; Hersh, L.B.
J. Biol. Chem. 267, 13505-13512, 1992
A>Title: Cloning a rat meprin cDNA reveals the enzyme is a heterodimer.
A>Reference number: A42908; MUID:92317075; PMID:1377685
A>Accession: A42908
A>Status: preliminary
A>Molecule type: mRNA
A>Residues: 1-668 <JOH>
A>Cross-references: UNIPROT:P28826
C>Note: sequence extracted from NCBI backbone (NCBIP:107784)
C>Superfamily: meprin; astacin homology; EGF homology; MAM homology
C>Keywords: heterodimer; hydrolase; metalloproteinase; zinc
F>72-258/Domain: astacin homology <AST>
F>261-430/Domain: MAM homology <MAM>
F>153,157,163,212/Binding site: zinc (His, His, Tyr) #status predicted
F>154/Active site: Glu #status predicted

Query Match          5.0%; Score 132.5; DB 1; Length 668;
Best Local Similarity 24.2%; Pred. No. 0.061;
Matches 43; Conservative 31; Mismatches 55; Indels 49; Gaps 7;
```

Qy	276	IWKISDFARKLQEAVAGRIPAISPAPFYSTRYKMKCLRIYLNGDGTGRGTHLSLFFVVM	335
		: : : : :	
Db	432	IWHQNFTQLD-----GGQTIVTSPPPYSKK-GYAFQINLDLTSP-----TNVGLYFHLL	480
		: : : : :	
Qy	336	KGPNDALLRWPFN-QKYTLMLDN-----NREHY-----	364
		: : : : :	
Db	481	SGANDDLQWCPMQQATWTLLDNPDIRQMNSQRSITTDPKWTDNGSYLWDSPSKVG	540
		: : : : :	
Qy	365	IDAFPEDVTSSSFORPVDNMNIASGCLFCPSVKSMKAKNYSVRDDAIFKAIVDTGL	432
		: : : : :	
Db	541	VEAFPNPTQTSRRG-----GVGTSVFITQRRLKSREFLGDDGVYILLTVEDISHL	591
		: : : : :	

Search completed: November 10, 2004, 16:29:00
Job time : 42 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

CM protein - protein search, using sw model

Run on: November 10, 2004, 16:11:42 ; Search time 195 Seconds
(without alignments)
1245.170 Million cell updates/sec

Title: US-10-018-030B-2

Perfect score: 2211

Sequence: 1 MAAASVTPFSGLELLQPGFS.....NSVVRDFAIFKAIYDLTGL 422

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2168	98.1	500	2 Q72337	Q72337 homo sapien
2	2155.5	97.5	501	1 TRA2 HUMAN	Aah4662 homo sapien
3	2155.5	97.5	501	2 AAH4662	Aat27320 homo sapi
4	2155.5	97.5	501	1 AAT27320	P39429 mus musculu
5	1914.5	86.6	501	1 TRA2 MOUSE	Q8C6X9 mus musculu
6	1914.5	86.6	501	2 Q8C6X9	Q8C6Q7 mus musculu
7	1910.5	86.4	501	2 Q8C6Q7	Q7T2X2 oncorhynch
8	1256	56.8	526	2 Q7T2X2	Q90WT6 carassius a
9	1149.5	52.0	501	2 Q90WT6	Q6NRN3 xenopus lae
10	1131.5	51.2	461	2 Q6NRN3	Aah70713 xenopus l
11	1131.5	51.2	461	1 AAH70713	Q13077 homo sapien
12	733.5	33.2	416	1 TRA1 HUMAN	Q60803 mus musculu
13	730	33.0	567	1 TRA3 MOUSE	Q8C6Z8 mus musculu
14	729	33.0	409	2 Q8C6Z8	P39428 mus musculu
15	727	32.9	409	1 TRA1 MOUSE	Q13114 homo sapien
16	717.5	32.5	568	1 TRA3 HUMAN	Q6DEG0 brachydanio
17	690	31.2	573	2 Q6DEG0	Q00463 homo sapien
18	687.5	31.1	557	1 TRA5 HUMAN	Q8AW99 oncorhynch
19	678	30.7	576	2 Q8AW99	Q805B1 gallus gall
20	669	30.3	557	2 Q805B1	P70191 mus musculu
21	664	30.0	558	1 TRA5 MOUSE	Q7T1X2 brachydanio
22	498	22.5	470	2 Q7T1X2	Aah5969 brachydan
23	498	22.5	470	1 AAH5969	Q9BUZ4 homo sapien
24	495	22.4	470	1 TRA4 HUMAN	Q6DFG9 xenopus lae
25	487	22.0	470	2 Q6DFG9	Q8BBD9 m mus muscu
26	486	22.0	470	2 Q8BBD9	Q6DEV2 xenopus tro
27	478	21.6	470	2 Q6DEV2	Q7T1K1 brachydanio
28	471	21.3	478	2 Q7T1K1	Q61382 mus musculu
29	454.5	20.6	470	1 TRA4 MOUSE	Q70617 hydractinia
30	430.5	19.5	409	2 Q70617	CAE88928 hydractin
31	430.5	19.5	409	2 CAE88928	

32	429	19.4	530	2 Q6P9M0	Q6P9M0 mus musculu
33	429	19.4	530	2 AAH60705	Aah60705 mus muscu
34	427	19.3	296	2 Q8QUJ9	Q8QUJ9 infectious
35	424	19.2	530	1 TRA6 MOUSE	P70196 mus musculu
36	419	19.0	556	2 Q6DJN2	Q6DJN2 xenopus lae
37	410	18.5	522	1 TRA6 HUMAN	Q9Y4K3 homo sapien
38	400.5	18.1	352	2 Q9SLK1	Q9SLK1 macaca fasc
39	397	18.0	542	2 Q7SXX1	Q7SXX1 brachydanio
40	395	17.9	462	2 Q9BIW7	Q9BIW7 caenorhabdi
41	395	17.9	509	2 Q62248	Q62248 caenorhabdi
42	393	17.8	542	2 Q6IWL4	Q6IWL4 brachydanio
43	393	17.8	542	2 AAT37634	Aat37634 brachydan
44	326.5	14.8	402	2 Q7PJX7	Q7PJX7 anopheles g
45	326.5	14.8	484	2 Q7Q116	Q7Q116 anopheles g

ALIGNMENTS

RESULT 1

Q72337	PRELIMINARY;	PRT;	500 AA.
AC Q72337	Q72337		
DT 01-OCT-2003	(Tremblrel. 25, Created)		
DT 01-OCT-2003	(Tremblrel. 25, Last sequence update)		
DT 01-MAR-2004	(Tremblrel. 26, Last annotation update)		
DE	Hypothetical protein DKPZp686H1465 (Fragment).		
GN	Name=DKPZp686H1465;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Human endometrium;		
RA	Ottewaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weil B.,		
RA	Amid C., Osanger A., Fobo G., Han M., Wiemann S.;		
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.		
CC	-!- SIMILARITY: Contains 1 RING-type zinc finger.		
DR	EMBL; BX538160; CAD98040.1;		
DR	GO; GO:0000151; C:ubiquitin ligase complex; IEA.		
DR	GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.		
DR	GO; GO:0008270; F:zinc ion binding; IEA.		
DR	GO; GO:0006567; P:protein ubiquitination; IEA.		
DR	InterPro; IPR002083; MATH.		
DR	InterPro; IPR001841; Znf_ring.		
DR	InterPro; IPR001293; Znf_TRAF.		
DR	Pfam; PF00917; MATH; 1.		
DR	Pfam; PF00097; ZF-C3HC4; 1.		
DR	Pfam; PF02176; ZF-TRAF; 1.		
DR	SMART; SM00061; MATH; 1.		
DR	SMART; SM00184; RING; 1.		
DR	PROSITE; PS00144; MATH; 1.		
DR	PROSITE; PS00518; ZF_RING_1; 1.		
DR	PROSITE; PS00089; ZF_RING_2; 1.		
DR	PROSITE; PS00445; ZF_TRAF; 1.		
KW	Hypothetical protein; Metal-binding; Zinc; Zinc-finger.		
FT	NON TER		
SQ	SEQUENCE 500 AA; 55253 MW; AC9B3D7DDC4F25B3 CRC64;		

Query Match	98.1%;	Score 2168;	DB 2;	Length 500;
Best Local Similarity	88.4%;	Pred. No. 1.5e-144;		
Matches 421;	Conservative 0;	Mismatches 1;	Indels 54;	Gaps 1;
QY	1	MAAASVTPFSGLELLQPGFSKTLTGKLEAKYLSACRNVLRRPFOACGHRYSFCFLAS	60	
Db	25	MAAASVTPFSGLELLQPGFSKTLTGKLEAKYLSACRNVLRRPFOACGHRYSFCFLAS	84	
QY	61	ILSSGPQNCACVHEGIIYEELGSIILESSAPPDNAARVESLPVCFSDGCTWKGTKE	120	
Db	85	ILSSGPQNCACVHEGIIYEELGSIILESSAPPDNAARVESLPVCFSDGCTWKGTKE	144	
QY	121	YE-----FQDH	126	

Db 145 YSCEHGRCPMLTECPACKGLVRLGEXERHLEHECPRESLSCHRCAPCGADVKKQDH 204
QY 127 VTKCKRCVPCRFHFAIGCTVEGSKQOEHEVQWMLREHLAMLLSVLEAKPLLDGQSHAG 186
Db 205 VTKCKRCVPCRFHFAIGCTVEGSKQOEHEVQWMLREHLAMLLSVLEAKPLLDGQSHAG 264
QY 187 SELLQRCSEKKTATFENIVCLNREVERVAMTAACSCROHRLDQDKIEALSQVQOLE 246
Db 265 SELLQRCSEKKTATFENIVCLNREVERVAMTAACSCROHRLDQDKIEALSQVQOLE 324
QY 247 RSIGLKDLAMADLEQKVLMEASTYDGVFIWKISDFARKLQEAAGVAGRIPAIFSPAFYTSR 306
Db 325 RSIGLKDLAMADLEQKVLMEASTYDGVFIWKISDFARKLQEAAGVAGRIPAIFSPAFYTSR 384
QY 307 GYKNCRLIYNGDGTGRGTHLSLFFVVMKGNPDALLRPENQKVTMLLDONNREHVID 366
Db 385 GYKNCRLIYNGDGTGRGTHLSLFFVVMKGNPDALLRPENQKVTMLLDONNREHVID 444
QY 367 AFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEAKNSYVRDDAIFKAIIVDLTGL 422
Db 445 AFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEAKNSYVRDDAIFKAIIVDLTGL 500
RESULT 2
ID TRAF2 HUMAN STANDARD; PRT; 501 AA.
AC Q12933; O96NT2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE TNF receptor associated factor 2 (Tumor necrosis factor type 2)
DE Receptor associated protein 3)
GN Name=TRAF2; Synonyms=TRAF3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP MEDLINE=95366958; PubMed=7639698;
RX Song H.Y., Donner D.B.;
RT "Association of a RING finger protein with the cytoplasmic domain of
RT the human type-2 tumour necrosis factor receptor.";
RL Biochem. J. 309:825-829 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamiyama M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Yanazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiyama S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Moniyama H., Sato N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Sato T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45 (2004).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, Fetal brain, Kidney, Leukocyte, and Stomach;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE OF 201-501 FROM N.A., AND INTERACTIONS WITH TRAF1 AND
RP TNFRSF1B.
RX MEDLINE=94349371; PubMed=80669916;
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692 (1994).
RN [5]
RP REVIEW.
RX MEDLINE=21278352; PubMed=11384837;
RA Wajant H., Henkler F., Scheurich P.;
RT "The TNF-receptor-associated factor family: scaffold molecules for
RT cytokine receptors, kinases and their regulators.";
RL Cell. Signal. 13:389-400 (2001).
RN [6]
RP REVIEW.
RX MEDLINE=21519158; PubMed=11607847; DOI=10.1038/sj/onc/1204788;
RA Bradley J.R., Pober J.S.;
RT "Tumor necrosis factor receptor-associated factors (TRAFs).";
RN Oncogene 20:6482-6491 (2001).
RN [7]
RP INTERACTION WITH TNFRSF8.
RX MEDLINE=96195221; PubMed=8627180;
RA Lee S.Y., Park C.G., Choi Y.;
RT "T cell receptor-dependent cell death of T cell hybridomas mediated by
RT the CD30 cytoplasmic domain in association with tumor necrosis factor
RT receptor-associated factors.";
RL J. Exp. Med. 183:669-674 (1996).
RN [8]
RP INTERACTION WITH TNFRSF14.
RX MEDLINE=96323205; PubMed=8710854;
RA Rothe M., Xiong J., Shu H.-B., Williamson K., Goddard A.,
RA Goeddel D.V.;
RT "I-TRAF is a novel TRAF-interacting protein that regulates TRAF-
RT mediated signal transduction.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:8241-8246 (1996).
RN [9]
RP INTERACTION WITH TNFRSF14.
RX MEDLINE=97298041; PubMed=9153189;
RA Hsu H., Solovayev I., Colombero A., Elliott R., Kelley M., Boyle W.J.;
RT "ATAR, a novel tumor necrosis factor receptor family member, signals

through TRAF2 and TRAF5.";
 RL J. Biol. Chem. 272:13471-13474 (1997).
 RN [10]
 RP INTERACTION WITH TRIP.
 RX MEDLINE=97258620; PubMed=9104814;
 RA Lee S.Y., Lee S.Y., Choi Y.;
 RT "TRAF-interacting protein (TRIP): a novel component of the tumor
 RT necrosis factor receptor (TNFR) - and CD30-TRAF signaling complexes
 RT that inhibits TRAF2-mediated NF-kappaB activation.";
 RL J. Exp. Med. 185:1275-1285 (1997).
 RN [11]
 RP INTERACTION WITH MAP3K14.
 RX MEDLINE=97172277; PubMed=9020361;
 RA Malinin N.L., Boldin M.P., Kovalenko A.V., Wallach D.;
 RT "MAP3K-related kinase involved in NF-kappaB induction by TNF, CD95 and
 RT IL-1.";
 RL Nature 385:540-544 (1997).
 RN [12]
 RP INTERACTION WITH TNFRSF5.
 RX MEDLINE=98384149; PubMed=9718306; DOI=10.1021/bi981067g;
 RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
 RA Kehry M.R.;
 RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)
 RT interactions: regulation of CD40 signaling through multiple TRAF
 RT binding sites and TRAF hetero-oligomerization.";
 RL Biochemistry 37:11836-11845 (1998).
 RN [13]
 RP INTERACTION WITH RIPK2.
 RX MEDLINE=98381580; PubMed=9705938;
 RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
 RA Mattmann C., Tschoep J.;
 RT "Identification of CARDIAK, a RIP-like kinase that associates with
 RT caspase-1.";
 RL Curr. Biol. 8:885-888 (1998).
 RN [14]
 RP INTERACTION WITH TNFRSF7.
 RX MEDLINE=98355635; PubMed=9692890;
 RX DOI=10.1002/ISICI.1521-4141(199807)28:07<2208::AID-IMMU2208>3.0.CO;2-L;
 RA Gravelstein L.A., Ansen D., Boes M., Calvo C.R., Kruisbeek A.M.,
 RA Borst J.;
 RT "The TNF receptor family member CD27 signals to Jun N-terminal kinase
 RT via Traf-2.";
 RL Eur. J. Immunol. 28:2208-2216 (1998).
 RN [15]
 RP INTERACTIONS WITH TNFRSF4 AND TNFRSF9.
 RX MEDLINE=98078711; PubMed=9418902;
 RA Arch R.H., Thompson C.B.;
 RT "4-1BB and OX40 are members of a tumor necrosis factor (TNF)-nerve
 RT growth factor receptor subfamily that bind TNF receptor-associated
 RT factors and activate nuclear factor kappaB.";
 RL Mol. Cell. Biol. 18:558-565 (1998).
 RN [16]
 RP INTERACTION WITH TNFRSF4.
 RX MEDLINE=98157982; PubMed=9488716;
 RA Kawamata S., Hori T., Imura A., Takaori-Kondo A., Uchiyama T.;
 RT "Activation of OX40 signal transduction pathways leads to tumor
 RT necrosis factor receptor-associated factor (TRAF) 2- and TRAF5-
 RT mediated NF-kappaB activation.";
 RL J. Biol. Chem. 273:5808-5814 (1998).
 RN [17]
 RP INTERACTION WITH TNFRSF11A.
 RX MEDLINE=98447691; PubMed=9774460;
 RA Wong B.R., Josien R., Lee S.Y., Vologodskaya M., Steinman R.M.,
 RA Choi Y.;
 RT "The TRAF family of signal transducers mediates NF-kappaB activation
 RT by the TRANCE receptor.";
 RL J. Biol. Chem. 273:28355-28359 (1998).
 RN [18]
 RP INTERACTION WITH TNFRSF9.
 RX MEDLINE=98270914; PubMed=9607925;
 RA Scoulli K., Lee S.Y., Camons J.B., Yeh W.C., Santana A.,
 RA Goldstein M.D., Borgia N., Defenedette M.A., Mak T.W., Choi Y.,
 RA Watts T.H.;

"CD28-independent, TRAF2-dependent costimulation of resting T cells by
 RT 4-1BB ligand.";
 RL J. Exp. Med. 187:1849-1862 (1998).
 RN [19]
 RP INTERACTION WITH MAP3K5.
 RX MEDLINE=98448103; PubMed=9774977;
 RA Nishitoh H., Saitoh M., Mochida Y., Takeda K., Nakano H., Rothe M.,
 RA Nishitoh H.;
 RT Query Match 97.5%; Score 2155.5; DB 1; Length 501;
 RT Best Local Similarity 84.0%; Pred. No. 1.2e-143; Indels 79; Gaps 1;
 RT Matches 421; Conservative 0; Mismatches 1;
 QY 1 MAASVTTPGSLLELLQPGFSKTLTGTLKLEAKYLSACRNVLRRPFOACGHRYSFCLAS 60
 DB 1 MAASVTTPGSLLELLQPGFSKTLTGTLKLEAKYLSACRNVLRRPFOACGHRYSFCLAS 60
 QY 61 ILSSGFQNCACVHEGIYEEGISILESSAPPDPAARREVSLEPAVCPDCTWKGLKE 120
 DB 61 ILSSGFQNCACVHEGIYEEGISILESSAPPDPAARREVSLEPAVCPDCTWKGLKE 120
 QY 121 YE----- 122
 DB 121 YESCHEGRCPLMLTECPACKGLVRLGEKHEHECPERSLSCHRCAPCCGADVKAHHE 180
 QY 123 -----FQDHVKTGCRVPCRFPHATGCTLETVEGEKQOHEVQWL 161
 DB 181 VCPKEPLTCDGCGKKKIPREKFQDHVKTGCRVPCRFPHATGCTLETVEGEKQOHEVQWL 240
 QY 162 REHLAMLSSVLEAKPLLDGSHAGSELQRCESLEKKTATFENIVCVLNEVERVANTA 221
 DB 241 REHLAMLSSVLEAKPLLDGSHAGSELQRCESLEKKTATFENIVCVLNEVERVANTA 300
 QY 222 EACSRQHRLDQDKIEALSSKQQQLERSIGLKDAMADLEQKLEMEASTYDGVFIWKISD 281
 DB 301 EACSRQHRLDQDKIEALSSKQQQLERSIGLKDAMADLEQKLEMEASTYDGVFIWKISD 360
 QY 282 PARKLOEAVAGRIPAIFSPATRYGYKMCRLIYLNCDGTGRGTHLSLFFVWVKGPDA 341
 DB 361 FARKEQEAVAGRIPAIFSPATRYGYKMCRLIYLNCDGTGRGTHLSLFFVWVKGPDA 420
 QY 342 LLRWPFNQKVTMLLDQNNREHVIDAFRPDVTSSTSSFPVNDMNIAASCPFCPVSKMEA 401
 DB 421 LLRWPFNQKVTMLLDQNNREHVIDAFRPDVTSSTSSFPVNDMNIAASCPFCPVSKMEA 480
 RESULT 3
 AAH64662
 ID AAH64662 PRELIMINARY; PRT: 501 AA.
 AC AAH64662;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE TNF receptor-associated factor 2, isoform 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.D., Ussin T.B., Ioshiki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

[2]
SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Kidney;
RA MEDLINE=98129826; PubMed=9461607;
RX Brink R., Lodish H.F.;
RT "Tumor necrosis factor receptor (TNFR)-associated factor 2A (TRAF2A),
a TRAF2 splice variant with an extended RING finger domain that
inhibits TNFR2-mediated NF-kappaB activation.";
RL J. Biol. Chem. 273:4129-4134 (1998).
[3]
SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6;
RX MEDLINE=21173195; PubMed=11275257;
RA Grech A., Quinn R., Srinivasan D., Badoux X., Brink R.;
RT "Complete structural characterisation of the mammalian and Drosophila
TRAF genes: implications for TRAF evolution and the role of RING
finger splice variants.";
RL Mol. Immunol. 37:721-734 (2000).
[4]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Bahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[5]
INTERACTION WITH TRADD.
RX MEDLINE=96152659; PubMed=8565075;
RA Hsu H., Shu H.-B., Pan M.G., Goeddel D.V.;
RT "TRADD-TRAF2 and TRADD-FADD interactions define two distinct TNF
receptor 1 signal transduction pathways.";
RL Cell 84:299-308 (1996).
[6]
INTERACTION WITH TNFAIP3.
RX MEDLINE=96270609; PubMed=8692885;
RA Song H.Y., Rothe M., Goeddel D.V.;
RT "The tumor necrosis factor-inducible zinc finger protein A20 interacts
with TRAF1/TRAF2 and inhibits NF-kappaB activation.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6721-6725 (1996).
[7]
INTERACTION WITH TRAF1.
RX MEDLINE=97258620; PubMed=9104814;
RA Lee S.Y., Lee S.Y., Choi Y.;
RT "TRAF1-interacting protein (TRIP): a novel component of the tumor
necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes
that inhibits TRAF2-mediated NF-kappaB activation.";
RL J. Exp. Med. 185:1275-1285 (1997).
[8]
FUNCTION: Adapter protein and signal transducer that links members
of the tumor necrosis factor receptor family to different
signaling pathways by association with the receptor cytoplasmic
domain and kinases. Association to the receptor is also mediated
by the interaction with TRADD. Mediates activation of NF-kappa-B
and JNK and is involved in apoptosis. Isoform 2 does not seem to
mediate activation of NF-kappa-B but inhibits isoform 1 activity.
The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2
and BIRC3 to TNFRSF1B/TNFR2. Seems to be involved in IL-15
Zinc-finger.

CC signaling (By similarity).
CC SUBUNIT: Homotrimer (Probable). Heteromer with TRAF1. Binds to
CC TNFRSF1B/TNFR2, TNFRSF4 and TNFRSF5/CD40 (By similarity).
CC Associates with TNFRSF7/CD27, TNFRSF8/CD30, TNFRSF9/CD137,
CC TNFRSF11A/RANK, TNFRSF13B/TAC1, TNFRSF14, TNFRSF16/NGFR,
CC TNFRSF17/BCMA, TNFRSF18/AT1R, TNFRSF19/TROY, TNFRSF19L/RELT,
CC XEDAR, EDAR, IL15RA, TANK/ITRAF, RIPK2, TNK1, MAP3K14, MAP3K5,
CC MAP3K1, MAP4K2, CDK9, CSK, and TRAF and TNF receptor associated
CC protein TRAP2 (By similarity). Interacts with TNFAIP3. Binds to
CC TRADD. Interacts with BIRC2 and BIRC3 N-terminus. Interacts with
CC CYLD (By similarity).
CC SUBCELLULAR LOCATION: Cytoplasmic.
CC ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P39429-1; Sequence=Displayed;
CC Name=2; Synonyms=TRAF2A;
CC IsoId=P39429-2; Sequence=VSP_007402;
CC Note=No experimental confirmation available. On mRNA level, has
CC a significantly shorter half-life than isoform 1;
CC TISSUE SPECIFICITY: Isoform 1 and isoform 2 are expressed in
CC spleen, adipose tissues, skeletal muscles, thymus, testis, heart,
CC lung, brain. Isoform 2 is very weakly expressed in heart, lung and
CC brain.
CC DOMAIN: The coiled coil domain mediates homo- and hetero-
CC oligomerization.
CC DOMAIN: The MATH/TRAF domain binds to receptor cytoplasmic
CC domains.
CC PTM: Ubiquitinated; mediated by SIAH2 and leading to its
CC subsequent proteasomal degradation. Not ubiquitinated by SIAH1 (By
CC similarity).
CC SIMILARITY: Contains 1 RING-type zinc finger.
CC SIMILARITY: Contains 2 TRAF-type zinc fingers.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L35303; AAC37662.1; --
CC EMBL; AF027570; AAC3545.1; --
CC EMBL; AF233332; AAF59928.1; --
CC EMBL; AF233326; AAF59928.1; JOINED.
CC EMBL; AF233337; AAF59928.1; JOINED.
CC EMBL; AF233328; AAF59928.1; JOINED.
CC EMBL; AF233329; AAF59928.1; JOINED.
CC EMBL; AF233330; AAF59928.1; JOINED.
CC EMBL; AF233331; AAF59928.1; JOINED.
CC EMBL; BC003801; AAH03801.1; --
CC PIR; I61512; I61512.
CC HSP; O12933; 1CA9.
CC MGD; MGI:101635; Traf2
CC GO; GO:0005535; P:protein binding; IPI.
CC GO; GO:0006916; P:anti-apoptosis; NAS.
CC InterPro; IPR002083; MATH.
CC InterPro; IPR008974; Traf-like.
CC InterPro; IPR001841; Znf ring.
CC InterPro; IPR001293; Znf_TRAF.
CC Pfam; PF00917; MATH; 1.
CC Pfam; PF00097; Zf-C3HC4; 1.
CC Pfam; PF02176; ZF-TRAF; 1.
CC SMART; SM00061; MATH; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS00144; MATH; 1.
CC PROSITE; PS00518; ZF_RING_1; 1.
CC PROSITE; PS00089; ZF_RING_2; 1.
CC PROSITE; PS00145; ZF_TRAF; 2.
CC Alternative splicing; Apoptosis; Coiled coil; Repeat; Ubl conjugation;
CC Zinc-finger.
KW


```

FT ZN FING 34 73 RING-type.
FT ZN FING 124 180 TRAP-type 1.
FT ZN FING 177 233 TRAP-type 2.
FT DOMAIN 298 348 Coiled coil (Potential).
FT DOMAIN 351 496 MATH.
FT VARSPLIC 62 62 L -> LRCASIIIS (in isoform 2).
FT VARSPLIC 62 62 /FTID=VSP 007402.
SQ SEQUENCE 501 AA; 56026 MW; 043B391180365F10 CRC64;

Query Match 86.6%; Score 1914.5; DB 1; Length 501;
Best Local Similarity 74.3%; Pred. No. 1.2e-126;
Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAASVTTPGSLLELQPGFSKTLTGKLEAKYLCACRNVLRRPFOACGHRYSFCLAS 60
DB 1 MAASVTSPGSLLELQPGFSKTLTGKLEAKYLCACRNVLRRPFOACGHRYSFCLTS 60
QY 61 ILSSGPQACACVHGIVYEEGISILESSAPFDNAARVESLPAVCPDCTWKGTLKE 120
DB 61 ILSSGPQACACVHGIVYEEGISILESSAPFDNAARVESLPAVCPDCTWKGTLKE 120
QY 121 YE----- 122
DB 121 YSCEHGLCPFLTECPACKGLVLRLSEKHEHTEQECPKRSLSCQHCRAPCSHVDLEVHYE 180
QY 123 -----FQDHVKTGCRKVRPCRFHAGICLETVEGEKQHEVQWL 161
DB 181 VCPKPEPLTCDGCKKKIPRETQDHRVACSKRVLRCFHTVGCSEMVETENLQDHEQLRL 240
QY 162 REHLAMILLSSVLEAKPLGDOSHAGSELQRCESLEKKTATFENIVCVLREVERVAVTA 221
DB 241 REHLALLSSVLEAQAQSGTQNGVPELQRCQILEQKATFENIVCVLREVERVAVTA 300
QY 222 EACSRQHLDDQKIBALSSKVQQLERSIGLKDLMADLEQKVLMEASTYDGVFIWKISD 281
DB 301 EACSRQHLDDQKIBALSSKVQQLERSIGLKDLMADLEQKVLMEASTYDGVFIWKISD 360
QY 282 FARKLOEAVAGRIPAIFSPAFYTRYGYKGLRYLNGDGTGRGTHLSLFFVVMKGNDA 341
DB 361 FTRKQEAQVAGRTPAIFSPAFYTRYGYKGLRYLNGDGTGRGTHLSLFFVVMKGNDA 420
QY 342 LLRPFPNOKVTLMLLDONNRHVDIADRPDVTSSSFQRPVNDMMIASGCLFCFVPSKWEA 401
DB 421 LLQFPNOKVTLMLLDONNRHVDIADRPDVTSSSFQRPVNDMMIASGCLFCFVPSKWEA 480
QY 402 KNSVYRDDAIFIKAVDITGL 422
DB 481 KNSVYRDDAIFIKAVDITGL 501

RESULT 6
ID Q8C6X9 PRELIMINARY; PRT; 501 AA.
AC Q8C6X9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
DE library, clone: D830048A10 product: Tnf receptor-associated factor 2,
DE full insert sequence.
GN Name=Traf2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=9279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA the FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:11617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:11757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AK052934; BAC35209.1; -.
DR HSSP; Q12933; 1CA9.
DR MGD; MGI:101835; Traf2.
DR GO; GO:0001873; Cubiquitin ligase complex; IEA.
DR GO; GO:0004872; F-ubiquitin activity; IEA.
DR GO; GO:0004842; F-ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F-zinc ion binding; IEA.
DR GO; GO:0016567; P-protein ubiquitination; IEA.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf-like.
DR InterPro; IPR001841; Znf_Fing.
DR InterPro; IPR001293; Znf_TRAF.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR Pfam; PF02176; ZF-TRAF; 1.
DR SMART; SM00061; MATH; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.

```

```
DR PROSITE; PS50145; ZF TRAF; 2.  
KW Metal-binding; Receptor; Zinc; Zinc-finger.  
SQ SEQUENCE 501 AA; 56086 MW; 89DDCB17782BBF1F CRC64;  
  
Query Match 86.4%; Score 1914.5; DB 2; Length 501;  
Best Local Similarity 74.3%; Pred. No. 1.2e-126;  
Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;  
  
QY 1 MAAASVTPGSLLELPGSKTLGKLEAKYLCSACRNLVRPPFOACQGHYVCSFCLAS 60  
DB 1 MAAASVTPGSLLELPGSKTLGKLEAKYLCSACRNLVRPPFOACQGHYVCSFCLAS 60  
QY 61 ILSSGPNCAACVHEGIYEGISILSSSAFPDPAARREVESLPAYCPDGGCTWGTGLKE 120  
DB 61 ILSSGPNCAACVHEGIYEGISILSSSAFPDPAARREVESLPAYCPDGGCTWGTGLKE 120  
QY 121 YE----- 122  
DB 121 YESCHEGLCPFLTECPACKGLVRLSEKHHTHEQECPSKLSQCHQACRPSHVLDVHYE 180  
QY 123 -----FOCHKTCGKCRVPCRFHAIGCTETVEGEKQOEHEVQWL 161  
DB 181 VCPKFPITVDGCGKKIPRETQDHYRACSKCRVLCRFHTVGCSENVETENIQDHELQRL 240  
QY 162 REHLAMLLSVLEAKPLGDQSHAGSELLQRCESLEKKTATTENIVCVLNREVERVAVTA 221  
DB 241 REHLAMLLSVLEAKPLGDQSHAGSELLQRCESLEKKTATTENIVCVLNREVERVAVTA 221  
QY 222 EACSRHRLDODKTEALSSKVOQLERSIGLKDLAVADLSQKLEMASTYDGVFTWKISD 281  
DB 301 EACSRHRLDODKTEALSSKVOQLERSIGLKDLAVADLSQKLEMASTYDGVFTWKISD 360  
QY 282 FAKLQEAAGVGRIPAFIPSPATYSRYGVKVLRYLNGDGTGRGTHLSLFFVVMKGPND 341  
DB 361 FTRKQEAAGVGRIPAFIPSPATYSRYGVKVLRYLNGDGTGRGTHLSLFFVVMKGPND 420  
QY 342 LLEWPNQKVTMLLDNNREHVIDAFRDPDVTSSSPQRPVNDMTASGCLFCPVSKEA 401  
DB 421 LLEWPNQKVTMLLDNNREHVIDAFRDPDVTSSSPQRPVNDMTASGCLFCPVSKEA 480  
QY 402 KNSYVRDDAIFIKAIVDLTGL 422  
DB 481 KNSYVRDDAIFIKAIVDLTGL 501  
  
RESULT 7  
Q8CAQ7 PRELIMINARY; PRT; 501 AA.  
AC Q8CAQ7  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched  
DE library, clone:Al30081B14 product:Tnf receptor-associated factor 2,  
DE full insert sequence.  
GN Name=Traf2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P.; Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
  
RL Nature 409:685-690(2001).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Thymus;  
RC The FANTOM Consortium,  
RA "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20493974; PubMed=11042159;  
RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RL prepare full-length cDNA libraries for rapid discovery of new genes.";  
RN [5]  
RN Genome Res. 10:1617-1630(2000).  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K.; Itoh M.; Aizawa K.; Nagao S.; Sasaki N.; Carninci P.,  
RA Konno H., Akiyama J., Nishi K.; Kitsumi T.; Tashiro H.; Itoh M.,  
RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.,  
RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.,  
RA Fujiwara S.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Watahiki M.,  
RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsuura S.; Kawai J.,  
RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kita A.; Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RL sequencing pipeline with 384 multicapillary sequencer.";  
RN [6]  
RN Genome Res. 10:1757-1771(2000).  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Adachi J.; Aizawa K.; Akimura T.; Arakawa T.; Bono H.; Carninci P.,  
RA Fukuda S.; Furuno M.; Hanagaki T.; Hara A.; Hashizume W.,  
RA Hayashida K.; Hayatsu N.; Hiramoto K.; Hiraoka T.; Hirozane T.,  
RA Hori F.; Imokawa K.; Ishii Y.; Itoh M.; Kagawa I.; Kasukawa T.,  
RA Kato H.; Kawai J.; Kojima Y.; Kondo S.; Konno H.; Kouda M.; Koya S.,  
RA Kurihara C.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.,  
RA Nishi K.; Nomura K.; Numazaki R.; Ohno M.; Ohsato N.; Okazaki Y.,  
RA Saito R.; Saitoh H.; Sakai C.; Sakai K.; Sakazume N.; Sano H.,  
RA Sasaki D.; Shibata K.; Shinagawa A.; Shiraki T.; Sogabe Y.; Tagami M.,  
RA Tagawa A.; Takahashi F.; Takaku-Akai H.; Takeda Y.; Tanaka I.,  
RA Tomaru A.; Toya T.; Yasunishi A.; Muramatsu M.; Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
DR EMBL; AK038136; BAC29937.1; -.  
DR HSSP; Q12933; 1CA9.  
DR MGD; MGI:101835; Traf2.  
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0016567; P:protein ubiquitination; IEA.  
DR InterPro; IPR002083; MATH.  
DR InterPro; IPR008974; Traf-like.  
DR InterPro; IPR001841; Znf_fing.  
DR InterPro; IPR001293; Znf_TRAF.  
DR Pfam; PF00917; MATH; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR Pfam; PF02176; zf-TRAF; 1.  
DR SMART; SM00061; MATH; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS50144; MATH; 1.  
DR PROSITE; PS00518; ZF_RING_1; 1.  
DR PROSITE; PS00089; ZF_RING_2; 1.  
DR PROSITE; PS50145; ZF_TRAF; 2.  
KW Metal-binding; Receptor; Zinc; Zinc-finger.  
SQ SEQUENCE 501 AA; 56026 MW; EB219C117A935FEA CRC64;  
  
Query Match 86.4%; Score 1910.5; DB 2; Length 501;
```

```

Best Local Similarity 74.1%; Pred. NO. 2.2e-126;
Matches 371; Conservative 22; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAASVTPFSGLELLQPGFSKTLTGKLEAKYLCACNVLRPFQACGHRYSFCLAS 60
Db 1 MAASVTPFSGLELLQPGFSKTLTGKLEAKYLCACNVLRPFQACGHRYSFCLAS 60
QY 61 ILSSGPQCAACVHGIYEEGISELESSAPFDPNAARREVSLEPAVCPDGTWKGLKE 120
Db 61 ILSSGPQCAACVHGIYEEGISELESSAPFDPNAARREVSLEPAVCPDGTWKGLKE 120
QY 121 YE----- 122
Db 121 YESCHEGLCPFLTECPACKGLVRLSEKHEHTEQECPRKRSLSOCHCRAPCSHVLDLVHYE 180
QY 123 -----FQDHVKTGCKRVPFCRFAIGCLETVEGEKQOHEVQWL 161
Db 181 VCKPPLTCDCGCKKKIPRETQDHVRAKSCRVLCRFHTVGCSEMVETENLQDHELQRL 240
QY 162 REHLAHLSSVLEAKPLGDQSHAGSELLORCESLEKKTATFENIVCLNREVERVAVTA 221
Db 241 REHLAHLSSVLEAKPLGDQSHAGSELLORCESLEKKTATFENIVCLNREVERVAVTA 300
QY 222 EACSRQHLDDKIPALSKVKQLERSIGLKDAMADLEQVLEMEASTYDGVFIWKISD 281
Db 301 EACSRQHLDDKIPALSKVKQLERSIGLKDAMADLEQVLEMEASTYDGVFIWKISD 360
QY 282 FARKLOEAVAGRIPAIFSPAFYTSRYGYKCLIRYLNQDGTGRGTHLSLFFVVMKGNDA 341
Db 361 FTRKQEAQVAGRTAIFSPAFYTSRYGYKCLIRYLNQDGTGRGTHLSLFFVVMKGNDA 420
QY 342 LLRWPFNKQVTLMLLDONNREHVIDAFRDPVTSSSFQRPVNDMNIASGCLFCFVSKWEA 401
Db 421 LLRWPFNKQVTLMLLDONNREHVIDAFRDPVTSSSFQRPVNDMNIASGCLFCFVSKWEA 480
QY 402 KNSYVRDDAIFKAIVDLTGL 422
Db 481 KNSYVRDDAIFKAIVDLTGL 501

RESULT 8
QY72X2 PRELIMINARY; PRT; 526 AA.
ID QY72X2
AC QY72X2
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Tumor necrosis factor receptor associated factor 2.
GN Name=TRAF2;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]_TaxID=8022;
RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Zou J., Zhang Y., Secombes C.J.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AJ548839; CAD59021.2;
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002083; MATH_
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF000917; MATH; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF02176; zf-TRAF; 2.

Best Local Similarity 56.8%; Score 1256; DB 2; Length 526;
Best Local Similarity 47.5%; Pred. No. 3.4e-80;
Matches 250; Conservative 68; Mismatches 100; Indels 108; Gaps 5;

QY 4 ASVTPFSGLELLQPGFSKTLTGKLEAKYLCACNVLRPFQACGHRYSFCLAS 63
Db 2 ARISLP-SLDLSLPRIPOSLAVSVEAKYQCCQCHVLRKPVQACGHRFCVKFKLTS 60
QY 64 SGPQCAACVHGIYEEGISELESSAPFDPNAARREVSLEPAVCPDGTWKGLKE- 122
Db 61 SGPKCEACRQEBIYEEPQSILNSNEAFDPNAAGREIASLPAKCISEGCSWTGCIKEYA 120
QY 123 ----- 122
Db 121 QHEGKDYERVPCETQVLLRSEKERHNERECEARTLNCKYKVSFNFKEIKAHDEICQ 180
QY 123 -----FQDHVKTGCKRVPFCRFAIGCLETVEGEKQOHEVQWLREH 164
Db 181 KFPMQCKGCKKKIPREKFLDHSRCAKSKTACPFSEVGCKVIIDNGKHSDEQTSVNEH 240
QY 165 LAMLSSVLEAK-----PLIGD-QSHAGSELLORCE-----SL 196
Db 241 LRLLATLSLVLQRPAPGLCEWQEDSGGLGRAPEDGATAAATDGGAAASQGTGL 300
QY 197 EKTATFENIVCLNREVERVAVTAACSRQHLDDKIEALSSKVKQLERSIGLKDAM 256
Db 301 DHKVRALENIVCLNREVERVAVTAACSRQHLDDKIEALSSKVKQLERSIGLKDAM 360
QY 257 ADLEQVLEMEASTYDGVFIWKISDFARKLOEAVAGRIPAIFSPAFYTSRYGYKCLIRY 316
Db 361 AETDQTLRELQCTFDGVFVWKIADFSSRRQDAVAGRTAPAMFSPAFYTSRYGYKCLIRY 420
QY 317 LNGDGTGRGTHLSLFFVVMKGNDAALLRPFNQKVTLMLLDQNNREHVIDAFRDPVTSS 376
Db 421 LNGDGTGRGTHLSLFFVVMKGNDAALLRPFNQKVTLMLLDQNNREHVIDAFRDPVTSS 480
QY 377 FORPVNDMNIASGCLFCFVSKWEAKNSYVRDDAIFKAIVDLTGL 422
Db 481 FLRPVNDMNIASGCLFCFVSKWEAKNSYVRDDAIFKAIVDLTGL 526

RESULT 9
QY90WT6 PRELIMINARY; PRT; 501 AA.
ID QY90WT6
AC QY90WT6
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor associate factor-2.
GN Name=traf2;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]_TaxID=7957;
RP SEQUENCE FROM N.A.
RA Wang T., Secombes C.J.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AJ297860; CAC82653.1; -.
DR HSSP; Q12933; 1C2Y.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.

```

GO: GO:0004842; F-ubiquitin-protein ligase activity; IEA.
GO: GO:0008270; P-zinc ion binding; IEA.
GO: GO:0016567; P-zinc ion binding; IEA.
InterPro: IPR002083; MATH.
InterPro: IPR006974; Traf-like.
InterPro: IPR001841; Znf_Traf.
InterPro: IPR001293; MATH.
Pfam: PF00917; MATH; 1.
Pfam: PF00097; ZF-C3HC4; 1.
Pfam: PF02176; ZF-TRAF; 2.
SMART: SM00061; MATH; 1.
SMART: SM00184; RING; 1.
PROSITE: PS0144; MATH; 1.
PROSITE: PS0089; ZF RING 2; 1.
PROSITE: PS0145; ZF TRAF; 2.
KW Metal-binding; Receptor; Zinc; Zinc-finger.
SQ SEQUENCE 501 AA; 56503 MW; DE0ED0F8D9DC287 CRC64;

Query Match 52.0%; Score 1149.5; DB 2; Length 501;
Best Local Similarity 47.8%; Pred. No. 1e-72;
Matches 226; Conservative 60; Mismatches 84; Indels 105; Gaps 4;

QY 2 AAASVTPPGSLELLQPGFKTLGTLKLEAKYLCSACRNVLRRPFOAQCCHRYCSFCLASI 61
Db 13 AMARPSPSSLDSTLPGISREVLVSMEPKYQCOQCKEILRPFQACCHRCVFCFKQL 72
QY 62 LSSGPONCAACVHEGIYEGISILESSAFPDPNAARREVESLPVPCSDGCTWKGTILKEY 121
Db 73 TSSGPIPCACRAEGIFEEAMSLNITVAPPDPAARREIDSLPAKCPNDGCSWGLTKDY 132
QY 122 E----- 122
Db 133 EGGHGRCDPFRVCKACQAVILLSEKDRHRECEARTLNCKYKVTFNPKYKAHDEI 192
QY 123 -----FQDHVTKCGKRVCFRFAIGCTLVGEGKQHEVQWLRL 162
Db 193 CQKFPMPQCKDCGKKIPREKFOHTKSCAKXSACQFSEIGCRAVVDNGKQHEGQTSVM 252
QY 163 EHLAMLLSSVLEAKPLIGD-----QSHAGSELLORCE-----SLE 197
Db 253 EHLRLML-SVLSVRIRAEAGAGQWSDSLGLYRGPEAPPAGPNAANAGRGPGVQ 311
QY 198 KKTATFENIVCVLNREVERVAMTAECRSQHRLDQDKIEALSSKVOQLERSIGLKDLAMA 257
Db 312 QKVTALENIVCVLNREVERVAMTAECRSQHRLDQDKIEALSSKVOQLERSIGLKDLAMA 371
QY 258 DLQKVLMEASTYDGVFWIKISDPARKLOEAVAGRIPIAFSPAFYTSRYGNMCLRIYL 317
Db 372 ESQSLRELQFCYTDGVFWIKIADFRRRQDAVGRAPAMFSPAFYSSKYGYKMLRLYL 431
QY 318 NGDGTGRGTHLSLFFVVMKGPNDALLRWPFNOKVTMLLDQNNRHHVIDAFRPDV 372
Db 432 NGDGTGRGTHLSLFFVVMKGPNDALLRWPFNOKVTMLLDQNNRHHVIDAFRPDI 486

RESULT 10
Q6NRN3
ID Q6NRN3 PRELIMINARY; PRT; 461 AA.
AC Q6NRN3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MG83471 protein.
GN Name=MG83471;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22386257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udoin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
"Genetic and genomic tools for Xenopus research: The NIH Xenopus
Initiative";
Dev. Dyn. 225:384-391(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Strausberg R.;
Submitted (Mar-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL: BC070713; AAH70713.1; -;
DR InterPro: IPR002083; MATH.
DR InterPro: IPR008974; Traf-like.
DR InterPro: IPR001841; Znf_Traf.
DR InterPro: IPR001293; Znf_Traf.
DR Pfam: PF00097; ZF-C3HC4; 1.
DR Pfam: PF02176; ZF-TRAF; 2.
DR PROSITE: PS0144; MATH; 1.
DR PROSITE: PS0089; ZF RING 2; 1.
DR PROSITE: PS0145; ZF TRAF; 2.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 461 AA; 51826 MW; 9981DC4C003C321D CRC64;

Query Match 51.2%; Score 1131.5; DB 2; Length 461;
Best Local Similarity 49.1%; Pred. No. 1.7e-71;
Matches 223; Conservative 56; Mismatches 70; Indels 105; Gaps 4;

QY 2 AAASVTPPGSLELLQPGFKTLGTLKLEAKYLCSACRNVLRRPFOAQCCHRYCSFCLASI 61
Db 7 AAASVSPGSLDLNQPFGPKKILGTGKLVKYLCSACRNLLRRPLQAQCCHRYCSHCFSKI 66
QY 62 LSSGPONCAACVHEGIYEGISILESSAFPDPNAARREVESLPVPCSDGCTWKGTILKEY 121
Db 67 ISSGPQKCAACIQEGLYEDGVSMLESSAFPDPNAARREVESLPAINVNCVTKGTIKEF 126
QY 122 E----- 122
Db 127 EVGHEGKQFVLPVCPVKALIRAIARDLNNRECPKRLNCRVKYLSVFPDVKVHDEI 186
QY 123 -----FQDHVTKCGKRVCFRFAIGCTLVGEGKQHEVQWLRL 162
Db 187 CPKPMTCGCGRKIKPREKFDHKGCGRCVFCRYAAVGAECWENDKCLEHKNFLA 246
QY 163 EHLA-----MLSSVLEAKPLI-----GDQSHAGS-----ELLQRCESL 196
Db 247 EHLAKVMDYIQDIKEQKDLRLRVGSLSVQGSFPGHNAFPVPENDSTKVKKILQKLDL 306
QY 197 EKKTATFENIVCVLNREVERVAMTAECRSQHRLDQDKIEALSSKVOQLERSIGLKDLMA 256

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Valalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [4]
 RP REVIEW
 RX MEDLINE=21278352; PubMed=11384837;
 RX Wajant H., Henkler F., Scheurich P.;
 RT "The TNF-receptor-associated factor family: scaffold molecules for
 RL cytokine receptors, kinases and their regulators.";
 RL Cell. Signal. 13:389-400(2001).
 RL [5]
 RP REVIEW
 RX MEDLINE=21519158; PubMed=11607847; DOI=10.1038/sj/onc/1204788;
 RX Bradley J.R., Fober J.S.;
 RT "Tumor necrosis factor receptor-associated factors (TRAFs).";
 RL Oncogene 20:6482-6491(2001).
 RL [6]
 RP INTERACTIONS WITH TRAF2 AND TNFRSF1B.
 RX MEDLINE=94349371; PubMed=8069916;
 RX Roche M., Wong S.C., Henzel W.J., Goeddel D.V.;
 RT "A novel family of putative signal transducers associated with the
 RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
 RL Cell 78:681-692(1994).
 RL [7]
 RP INTERACTION WITH TANK.
 RX MEDLINE=96323205; PubMed=8710854;
 RX Roche M., Xiong J., Shu H.-B., Williamson K., Goddard A.,
 RA Goeddel D.V.;
 RT "T-TRAF is a novel TRAF-interacting protein that regulates TRAF-
 RT mediated signal transduction.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8241-8246(1996).
 RL [8]
 RP INTERACTION WITH TNFRSF5.
 RX MEDLINE=98384149; PubMed=9718306; DOI=10.1021/b981067q;
 RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
 RA Kehry M.R.;
 RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)
 RT interactions: regulation of CD40 signaling through multiple TRAF
 RT binding sites and TRAF hetero-oligomerization.";
 RL Biochemistry 37:11836-11845(1998).
 RL [9]
 RP INTERACTION WITH RIPK2.
 RX MEDLINE=98381580; PubMed=9705938;
 RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
 RA Mattmann C., Tschopp J.;
 RT "Identification of CARDIAK, a RIP-like kinase that associates with
 RT caspase-1.";
 RL Curr. Biol. 8:885-888(1998).
 RL [10]
 RP INTERACTION WITH TNFRSF8.
 RX MEDLINE=96195221; PubMed=8627180;
 RA Lee S.Y., Park C.G., Choi Y.;
 RT "T cell receptor-dependent cell death of T cell hybridomas mediated by
 RT the CD30 cytoplasmic domain in association with tumor necrosis factor
 RT receptor-associated factors.";
 RL J. Exp. Med. 183:669-674(1996).
 RL [11]
 RP INTERACTION WITH RIPK2.
 RX MEDLINE=98307936; PubMed=9642260;
 RA McCarthy J.V., Ni J., Dixit V.M.;
 RT "RIP2 is a novel NF-kappaB-activating and cell death-inducing
 RT kinase.";
 RL J. Biol. Chem. 273:16968-16975(1998).
 RL [12]

RP INTERACTIONS WITH TNFRSF4 AND TNFRSF9.
 RX MEDLINE=98078711; PubMed=9418902;
 RA Arch R.H., Thompson C.B.;
 RT "4-1BB and Oxa40 are members of a tumor necrosis factor (TNF)-nerve
 RT growth factor receptor subfamily that bind TNF receptor-associated
 RT factors and activate nuclear factor kappaB.";
 RL Mol. Cell. Biol. 18:558-565(1998).
 RL [13]
 RP INTERACTION WITH TNFRSF9.
 RX MEDLINE=98270914; PubMed=9607925;
 RA Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
 RA Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
 RA Watts T.H.;
 RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by
 RT 4-1BB ligand.";
 RL J. Exp. Med. 187:1849-1862(1998).
 RL [14]
 RP INTERACTION WITH TNFRSF11A.
 RX MEDLINE=98447691; PubMed=9774460;
 RX Wong B.R., Josien R., Lee S.Y., Vologodskaja M., Steinman R.M.,
 RA Choi Y.;
 RT "The TRAF family of signal transducers mediates NF-kappaB activation
 RT by the TRANCE receptor.";
 RL J. Biol. Chem. 273:28355-28359(1998).
 RL [15]
 RP INTERACTION WITH TNFRSF18.
 RX MEDLINE=99156876; PubMed=10037686;
 RX Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
 RA Liu D., Wang S.-X., Kwon B.S.;
 RT "Identification of a novel activation-inducible protein of the tumor
 RT necrosis factor receptor superfamily and its ligand.";
 RL J. Biol. Chem. 274:6056-6061(1999).
 RL [16]
 RP INTERACTION WITH TNFRSF17.
 RX MEDLINE=20363816; PubMed=10903733;
 RA Hatzoglu A., Roussel J., Bourgeois M.-F., Rogier E., Madry C.,
 RA Inoue J.-I., Devergne O., Tsapis A.;
 RT "TNF receptor family member BCMA (B cell maturation) associates with
 RT TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and
 RT activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-
 RT activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RL [17]
 RP INTERACTION WITH TNFRSF19.
 RX MEDLINE=20270246; PubMed=10809768;
 RX Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
 RA "TJ", a novel member of the tumor necrosis factor receptor family,
 RT activates the c-Jun N-terminal kinase pathway and mediates caspase-
 RT independent cell death.";
 RL J. Biol. Chem. 275:15336-15342(2000).
 RL [18]
 RP INTERACTION WITH TNFRSF19L.
 RX MEDLINE=21213541; PubMed=11313261;
 RA Sica G.L., Zhu G., Tamada K., Liu D., Ni J., Chen L.;
 RT "RELT, a new member of the tumor necrosis factor receptor superfamily,
 RT is selectively expressed in hematopoietic tissues and activates
 RT transcription factor NF-kappaB.";
 RL Blood 97:2702-2707(2001).
 RL [19]
 RP INTERACTION WITH EDAR.
 RX MEDLINE=21264720; PubMed=11035039; DOI=10.1074/jbc.M008356200;
 RX Kumar A., Eby M.T., Sinha S., Jasmin A., Chaudhary P.M.;
 RA "The ectodermal dysplasia receptor activates the nuclear factor-
 RT kappaB, JNK, and cell death pathways and binds to ectodysplasin A.";
 RL J. Biol. Chem. 276:2668-2677(2001).
 RL CC -!- FUNCTION: Adapter protein and signal transducer that links members
 CC of the tumor necrosis factor receptor family to different
 CC signaling pathways by association with the receptor cytoplasmic
 CC domain and kinases. Mediates activation of NF-kappa-B and JNK and
 CC is involved in apoptosis. The TRAF1/TRAF2 complex recruits the
 CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2.
 CC -!- SUBUNIT: Homotrimer (Probable). Heteromer with TRAF2 and
 CC associates with TNFRSF1B/TNFR2 through TRAF2. Associates with

CC TNFRSF4, TNFRSF5/CD40, TNFRSF6/CD30, TNFRSF9/CD137,
CC TNFRSF11A/RANK, TNFRSF18/ATRA, TNFRSF17/BCMA, TNFRSF19/TROY,
CC TNFRSF19L/RELT, XEDAR, EDAR, Epstein-Barr virus ENFL1/LMP-1,
CC TANK/ITRAF, TRAF and RIPK2. Interacts with BIRC2 and BIRC3 N-terminus.
CC -!- DOMAIN: The coiled coil domain mediates homo- and hetero-oligomerization.
CC -!- DOMAIN: The MATH/TRAF domain binds to receptor cytoplasmic domains.
CC -!- SIMILARITY: Contains 1 MATH domain.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to a frameshift in position 111.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

Query Match 33.2%; Score 733.5; DB 1; Length 416;
Best Local Similarity 37.8%; Pred. No. 1.8e-43;
Matches 156; Conservative 65; Mismatches 109; Indels 83; Gaps 6;

QY 55 SFCLASILSSGPQN-----CAACVHEGIYEBGISTLESSAPFPDAAARVESLPAYCPS 109
Db 35 ALCCAGCLSENPRNGEDQICPKRGEDL-----QSISPGSLRLTQEKAPHEV--- 81
QY 110 DCTWKGTILKEYFDFDHVTKGCKRVPCHPAICGLEIVEGEKQEHVQWLREHLMLLL 169
Db 82 -----AEAGIGCFPAGVCGCFKSPQSQVQEHVTSQTSHLMLLL 120
QY 170 SSVLEAKPLLDQSHAGSELLQ-----CE----- 194
Db 121 GPMKWKARLGGLESGLPMALEQNLSDLOQAAVEVAGDLEVCYRAPCSQSEELALQH 180
QY 195 -----SLEKATATFNIVCLNREVERVAMTAECRSOHRLDQKIEALSKVQOOLE 246
Db 181 FMKEXLLAELEGKLVFNINAVLNKEVEAGSHALATSIHOSQDRIRLSLEQRVVELQ 240
QY 247 RSGIKDLAMADLEQVLEMASTYDGVFIWKISDFARKLEAVAGRIPAIFSPAFYTSR 306
Db 241 QTLAQDQALGKLESLMLMEASFGTLFWKINTVTRCHESACGRVTSVLSFPAFTAK 300
QY 307 YGYKCLRIYNGDGTGRGTHLSLFFVVMKGNPDALLRWPNQKVTMLLDQNNREHVID 366
Db 301 YGYKCLRLYLNGDGTGRGTHLSLFFVIMRGYDALLPWPFRNKTFTMLLDQNNREHAID 360
QY 367 AFRPDVTSSQRPVNDNINAGCPFCVSKMEA-KNSVYRDDAIFKAIQVD 418
Db 361 AFRPLSSASFQPSQSETNVSAGGCLFFPLSKQSPKHAYVYKDDTFLKICVE 413

RESULT 13

TRA3 MOUSE
ID TRA3 MOUSE STANDARD; PRT; 567 AA.
AC Q60803; Q62380;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE TNF receptor associated factor 3 (CD40 receptor associated factor 1)
DE (CRAF1) (TRAFAMN)
GN Name=Tra3; Synonyms=CRAF1, Trafam;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND INTERACTION WITH TNFRSF5.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498(1995).
RN [2]
RC SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=96299439; PubMed=8660894;
RA Wang X., Bornslaeger E.A., Haub O., Tomihara-Newberger C., Lomberg N.,

RA Dinulos M.B., Distche C.M., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Lacy E.;
RT "A candidate gene for the amionless gastrulation stage mouse mutation encodes a TRAF-related protein.";
RL Dev. Biol. 177:274-290(1996).
CC -!- FUNCTION: Adapter protein and signal transducer that links members of the tumor necrosis factor receptor family to different signaling pathways by association with the receptor cytoplasmic domain and kinases. Seems to be involved in activation of NF-kappa-B and JNK and in apoptosis. Is regulated by TANK/ITRAF which competes with TNFRSF5/CD40 for binding. Seems to play a role T-cell dependent immune responses (By similarity).
CC -!- SUBUNIT: Homotrimer (probable). Heteromer with TNFRSF3, TNFRSF4, TNFRSF8/CD30, TNFRSF17/BCMA and EDAR, MAP3K5, MAP3K14, and TRAF-interacting protein TRIP and TRAF and TNF receptor associated protein TRAF. Binds to TANK/ITRAF (By similarity).
CC -!- TISSUE SPECIFICITY: In adult, highest in brain. Also found in kidney, heart, thymus, spleen, lung, muscle, testis and ovary. Not found in liver.
CC -!- DEVELOPMENTAL STAGE: In the embryo, expressed from E6.5 with highest levels found between E11.5 and E13.5. At late stages of gestation, from E14.5, only low levels are detected.
CC -!- DOMAIN: The MATH/TRAF domain binds to receptor cytoplasmic domains.
CC -!- SIMILARITY: Contains 1 MATH domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 2 TRAF-type zinc fingers.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U21050; AAC52175.1; -;
DR EMBL; U33840; AAC52710.1; -;
DR PIR; I49272; I49272.
DR HSP; Q13114; 1FLX.
DR MGD; MGI:108041; Traf3.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf like.
DR InterPro; IPR001841; Znf_Ring.
DR InterPro; IPR001293; Znf_TRAF.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF02176; zf-TRAF; 2.
DR SMART; SM0061; MATH; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01444; MATH; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR PROSITE; PS0145; ZF_TRAF; 2.
KW Apoptosis; Coiled coil; Repeat; Zinc-finger.
FT ZN_FING 67 76 RING-type.
FT ZN_FING 134 189 TRAF-type 1.
FT ZN_FING 190 248 TRAF-type 2.
FT DOMAIN 266 337 Coiled coil (Potential).
FT DOMAIN 414 559 MATH.
FT CONFLICT 72 73 CE -> WQ (in Ref. 2).
FT CONFLICT 390 390 T -> M (in Ref. 2).
SQ SEQUENCE 567 AA; 64263 MW; 2522B343B41192DC CRC64;

Query Match 33.0%; Score 730; DB 1; Length 567;
Best Local Similarity 32.1%; Pred. No. 4.7e-43;
Matches 187; Conservative 80; Mismatches 131; Indels 184; Gaps 22;

QY 1 MAASVTPFGSLELLQ-----GFSKTLGLTKLEAKYLCISACNVLRRPFOA 47
Db 7 MDAAAGTLQNPPLKLPDRGAGSVLPVPGGYKEKFKVT-VEKVKCKEKLVLNCPKQT 65


```
QY 48 QCGHRYCSPCLASILSSGPONCAACVHEGIYERIGISILESSAPFPNAAARREVESLPAVC 107
Db 66 ECGRHFCESCMAALLSSSPKCTAC-QESIIRKDV-----FKDNCKREILALQVYC 116
QY 108 PSD--GCTWKGTL-----KEYEFO-----DHYK-----TC 130
Db 117 RNEGRGCAEOLTLGHLVHLKNCQFEELPCLPADCKEKVLKDLRDHVEKACKYREATC 176
QY 131 GKCR--VP-----CRFHAI 142
Db 177 SHCKSQVPMIKLOKHEDTDCPCVVVSCPHKCSVQTLRSLSAHLSECVNAPSTCSFKY 236
QY 143 GCLTEVEGEKQO--EHEVQWLRHLAML--LSSVLEAKPLIGDQSHAGSELLQRCESLXK 198
Db 237 CCV--FQGTNQQAHAESAASAVOHVLLKENSLEK-----VSLQN-ESVBK 293
QY 199 KTA--TFENIVCVLNREVER-----VAMTAEACS-----RQHR 229
Db 284 NKSIQSLHNGICSFETIERQKEMLRNBSKILHLQRVIDSQAELKELDKELRPPRQNW 343
QY 230 LDOD---KTEALSSKVOOLE-----RSIGLKDLAVADLEQ 261
Db 344 EEDSMKSSVESQNRVTELESVDKAGQAARNTGLLESQSLSHDQTLVSHDIRLADMDL 403
QY 262 KVLEMEASTVDGVFIWKIDFARKLOEAVAGRIPAFYTSRYGYKMCRLIYINGDG 321
Db 404 RFQVLETAGVINGVLIKIRDYKXKQEAQVNGKTLISYQPFYTGVEGYKWCARVINGDG 463
QY 322 TGEGLTHLSUFFVVKGNPNDALLRWPKNQKVTMLLDQ--NNREHVIDAFPPDVTSSFPQP 380
Db 464 MGKGTHTLSUFFVIMRGDEYDALLFPWPKQVKVTMLMDQSSRRHLGDAFPDPNSSFPPK 523
QY 381 VNDMNIASGCPPLPCPYSKMEAKNSYVRDDAIFIKAIVDLTGL 422
Db 524 TGEWNIASGCPVPVAVQTVLE-NGTYIKDDTIFIKIVDTSIDL 564

RESULT 14
Q8CE28 ID Q8CE28 PRELIMINARY; PRT; 409 AA.
AC Q8CE28
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:473249E14 product:Tnf receptor-associated factor 1,
DE full insert sequence.
GN Name-Trafi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA the FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
```

```
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076661;
RA Shibata K., Itoh M., Azawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Azawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK029135; BAC26315.1; --
DR HSP; Q12933.1CZY.
DR MGD; MGI:101836; Trafi.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50144; MATH; 1.
DR Receptor.
SQ SEQUENCE 409 AA; 45464 MW; ADD7F997169D9AAD CRC64;
Query Match 33.0%; Score 729; DB 2; Length 409;
Best Local Similarity 38.7%; Pred. No. 3.7e-43;
Matches 158; Conservative 62; Mismatches 112; Indels 76; Gaps 6;
QY 85 LESSSAPPDNARREVESLPAVCSDG----CTWKGTILKEYEPDQHVKTCKR----- 134
Db 1 MASSSAPDENEFGCPAPQCDSEPRVLCT--ACLSNLRDDEDRICPKCRADNLHP 58
QY 135 -----VPCRFHAIGCLTEVEGEKQCEHVQWLRHLAMLSSVLE 174
Db 59 VSPGSPLTQEKVHSDVAEAEIMCPFAGVCGSPKSPQSMQEHEATSOSSHLVLLAVLKE 118
QY 175 AKPLLGPQSHAGSELLOR-----CES----- 195
Db 119 WKSPFGSNLGSAPMALERNLSELQAAVEATGDLVDYCRAPCCESQEELALQHLVKEK 178
QY 196 ----LEKKTATFENIVCVLNREVERVAMTAEACSRHRLDQDKTEALSSKVOQLERSIGL 251
Db 179 LLAQLEEKLRVANIVAVLNKEVEASHLAASAASHQSLDREHLTSLQEVVEQLQTLAQ 238
QY 252 KDLAMADLEQKVLMEASTVDGVFIWKIDFARKLOEAVAGRIPAFYTSRYGYK 311
Db 60,770 full-length cDNAs."/>
```

Db 239 KDQVLGKLEHSLRLMEASFDGTFLWKITNTVKRCHESVCGRVSLSPAFYTKYGYKL 298
Qy 312 CLRIYLGNGDTCGRGHLSLFFVWVGKPNDAALLRWPNQKVTMLLDQNNREHVIDAFRPD 371
Db 299 CLRLYLNGDGGKTKHLSLFIIVMRGEYDALLPWFNRKVTFFMLLDQNNREHVIDAFRPD 358
Qy 372 VTSSSFQRPVNDMNIAASCPFLFCPVSKMEA-KNSYVRDDAIFIKAIYD 418
Db 359 LSSASFQRPQSETNVASGCPFLFFPLSKLQSPKHAYVKDDTWFCLKCIVD 406

RESULT 15
TRAF1_MOUSE
ID TRAF1_MOUSE STANDARD; PRT; 409 AA.
AC P39428;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE TNF receptor associated factor 1.
GN Name=Trafi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 123-135 AND 390-402, AND INTERACTIONS
RP WITH TRAF2 AND TNFRSF1B.
RX MEDLINE=94349371; PubMed=8069916;
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
RN [2]
RP INTERACTION WITH TRAF1.
RX MEDLINE=97258620; PubMed=9104814;
RA Lee S.Y., Choi Y.;
RT "TRAF1-interacting protein (TRIP): a novel component of the tumor
RT necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes
RT that inhibits TRAF2-mediated NF-kappaB activation.";
RL J. Exp. Med. 185:1275-1285(1997).
CC -!- FUNCTION: Adapter protein and signal transducer that links members
CC of the tumor necrosis factor receptor family to different
CC signaling pathways by association with the receptor cytoplasmic
CC domain and kinases. Mediates activation of NF-kappa-B and JNK and
CC is involved in apoptosis. The TRAF1/TRAF2 complex recruits the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2.
CC -!- SUBUNIT: Homotrimer (Probable). Heteromer with TRAF2 and
CC associates with TNFRSF1B/TNFR2 through TRAF2. Associates with
CC TNFRSF11A/RANK, TNFRSF18/AITR, TNFRSF17/BCMA, TNFRSF19/TROY,
CC TNFRSF19L/RELT, XEDAR, EDAR, TANK/ITRAF and RIPK2 (By similarity).
CC Interacts with BIRC2 and BIRC3 N-terminus (By similarity). Binds
CC TRAF1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- DOMAIN: The coiled coil domain mediates homo- and hetero-
CC oligomerization.
CC -!- DOMAIN: The MATH/TRAF domain binds to receptor cytoplasmic
CC domains.
CC -!- SIMILARITY: Contains 1 MATH domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L35302; AAC37663.1; -.
DR PIR: A54750; A54750.
DR HSP: Q12933; 1CZY.
DR MGD: MGI:101836; Trafi1.
DR InterPro: IPR002083; MATH.

DR InterPro: IPR008974; Traf_like.
DR Pfam: PF00917; MATH; 1.
DR SMART: SM00061; MATH; 1.
DR PROSITE: PS0144; MATH; 1.
KW Apoptosis; Coiled coil; Direct protein sequencing.
FT DOMAIN 167 256 Coiled coil (Potential).
FT DOMAIN 259 405 MATH.
SQ SEQUENCE 409 AA; 45464 MW; EBA7FBE5639FEDDF CRC64;
Query Match 32.9%; Score 727; DB 1; Length 409;
Best Local Similarity 38.5%; Pred. No. 5.1e-43;
Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;
Qy 85 IESSAFPPDNAARREVESLPAVCPDGG---CTWKGTLKEYEFQDHVTCGKCR----- 134
Db 1 MASSAPDENEFQCGPPAPCDPSEPRVLCCT--ACLSENLRDDEDRICPKCRADNLHP 58
Qy 135 -----VPCRFAIGCLETVEGEKQOEHEVQWLRHHLAMLSSVLE 174
Db 59 VSPGSLTQEKVHSDVAEAEIMCPFAGVCGSPQSMQHEATSQSHLYLLLAUKE 118
Qy 175 AKPLLDQDSHAGSELLQR-----CES----- 195
Db 119 WKSSPQSNLGSAPMALEENLSLQLAQAVEATGDLVDVCRAPCCESOEELALQHLVKEK 178
Qy 196 ----LEKKTATATTENIVCVLNREVERVAMTAEACSRQHLDDQDKIBALSSKYQOOLERSIGL 251
Db 179 LLAQLEEKLRVFPANTVAVLNKEVEASHLAAASHQSQLDREHLLSLQRYVVELOQTAAQ 238
Qy 252 KDLAMADLEOKVLEMEASTYDQVFTWKISDPARKQEAAGRIPAIFSPAFYTSRYGYKM 311
Db 239 KQOVIGKLEHSLRLMEASFDGTFLWKITNTVKRCHESVCGRVSLSPAFYTKYGYKL 298
Qy 312 CLRIYLGNGDTCGRGHLSLFFVWVGKPNDAALLRWPNQKVTMLLDQNNREHVIDAFRPD 371
Db 299 CLRLYLNGDGGKTKHLSLFIIVMRGEYDALLPWFNRKVTFFMLLDQNNREHVIDAFRPD 358
Qy 372 VTSSSFQRPVNDMNIAASCPFLFCPVSKMEA-KNSYVRDDAIFIKAIYD 418
Db 359 LSSASFQRPQSETNVASGCPFLFFPLSKLQSPKHAYVKDDTWFCLKCIVD 406

Search completed: November 10, 2004, 16:28:16
Job time : 200 secs